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version 5.1.3
3 - 2002 Compugen Ltd.

using sw model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	18	100.0	18	6	AX455555	AX455555 Sequence
5	17	94.4	18	6	AX104114	AX104114 Sequence
6	17	94.4	18	6	AX355358	AX355358 Sequence
7	17	94.4	24	6	AX463126	AX463126 Sequence
c 8	17	94.4	24	6	AX463127	AX463127 Sequence
9	13.2	73.3	37	6	AR089858	AR089858 Sequence
10	13.2	73.3	39	6	AR167631	AR167631 Sequence
c 11	13.2	73.3	48	6	AR151177	AR151177 Sequence
12	12.8	71.1	19	6	AX103935	AX103935 Sequence
c 13	12.8	71.1	19	6	AX131449	AX131449 Sequence
14	12.8	71.1	19	6	AX355385	AX355385 Sequence
15	12.8	71.1	41	6	AR169564	AR169564 Sequence
c 16	12.8	71.1	65	6	AX485786	AX485786 Sequence
c 17	12.8	71.1	83	6	AX241103	AX241103 Sequence
18	12.4	68.9	20	6	AR043709	AR043709 Sequence
c 19	12.4	68.9	40	6	AR172301	AR172301 Sequence
20	12.4	68.9	40	6	AR172302	AR172302 Sequence
c 21	12.4	68.9	65	6	AX485339	AX485339 Sequence
c 22	12.4	68.9	98	6	AR017618	AR017618 Sequence
c 23	12.4	68.9	98	6	AR094795	AR094795 Sequence
c 24	12.4	68.9	98	6	AR165454	AR165454 Sequence
25	12.2	67.8	27	6	AX283488	AX283488 Sequence
c 26	12.2	67.8	30	6	AX128526	AX128526 Sequence
27	12.2	67.8	39	6	A67624	A67624 Sequence 44
28	12.2	67.8	39	6	AR089762	AR089762 Sequence
c 29	12.2	67.8	46	6	E22537	E22537 Novel scree
c 30	12.2	67.8	49	9	HUMCFDELAA	M65196 Human cysti
c 31	12.2	67.8	98	9	HUMD4H12M3	D17247 Human HepG2
32	11.8	65.6	20	6	AX103939	AX103939 Sequence
33	11.8	65.6	20	6	AX355530	AX355530 Sequence
c 34	11.8	65.6	25	6	AX027188	AX027188 Sequence
c 35	11.8	65.6	25	6	AX027200	AX027200 Sequence
36	11.8	65.6	26	6	AR105706	AR105706 Sequence
c 37	11.8	65.6	35	6	AX155967	AX155967 Sequence
c 38	11.8	65.6	35	6	AX361817	AX361817 Sequence
39	11.8	65.6	36	6	I26200	I26200 Sequence 34
40	11.8	65.6	39	6	AR182122	AR182122 Sequence
41	11.8	65.6	40	6	AR169552	AR169552 Sequence
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43	11.8	65.6	51	6	AX162989	AX162989 Sequence
44	11.8	65.6	51	6	AX162991	AX162991 Sequence
45	11.8	65.6	51	6	AX162993	AX162993 Sequence

ALIGNMENTS

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DEFINITION Sequence 11 from Patent WO9832462.
ACCESSION A89789
VERSION A89789.1 GI:6738303
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 11 30-JUL-1998;

LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
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Db 1 AGCTATGACGTTCCAAGG 18

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DEFINITION Sequence 11 from Patent EP0855184.
ACCESSION A90876
VERSION A90876.1 GI:6739275
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Heeg,K.P. and Lipford,G.B.
TITLE Pharmaceutical composition comprising a polynucleotide and an antigen especially for vaccination
JOURNAL Patent: EP 0855184-A 11 29-JUL-1998;
HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES Location/Qualifiers
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Db 1 AGCTATGACGTTCCAAGG 18

RESULT 3
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DEFINITION Sequence 46 from Patent WO0122990.
ACCESSION AX105148
VERSION AX105148.1 GI:13921298
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hartmann,G.D., Bratzler,R.L. and Krieg,A.U.
TITLE Methods related to immunostimulatory nucleic acid-induced interferon
JOURNAL Patent: WO 0122990-A 46 05-APR-2001;
Coley Pharmaceutical Group, Inc. (US) ; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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source 1. .18
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Db 1 AGCTATGACGTTCCAAGG 18

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LOCUS AX455555 18 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 32 from Patent WO0222809.
ACCESSION AX455555
VERSION AX455555.1 GI:21714623
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bauer,S., Lipford,G. and Wagner,H.
TITLE Process for high throughput screening of cpg-based immuno-agonist/antagonist
JOURNAL Patent: WO 0222809-A 32 21-MAR-2002;
Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .18
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DEFINITION Sequence 306 from Patent WO0122972.
ACCESSION AX104114
VERSION AX104114.1 GI:13920311
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 306 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .18
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ACCESSION   AX355358
VERSION     AX355358.1  GI:18620026
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 386 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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Qy      2 GCTATGACGTTCCAAGG 18
          |||||||||||||||||
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LOCUS       AX463126                 24 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 9 from Patent WO0250108.
ACCESSION   AX463126
VERSION     AX463126.1  GI:21886107
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Marchal,G., Pescher,P. and Romain,F.
  TITLE     Immunogenic glycopeptides, screening, preparation and uses
  JOURNAL   Patent: WO 0250108-A 9 27-JUN-2002;
            PASTEUR INSTITUT (FR)
FEATURES             Location/Qualifiers
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                     /note="linker"
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 GCTATGACGTTCCAAGG 18
          |||||||||||||||||
Db      4 GCTATGACGTTCCAAGG 20


RESULT 8
AX463127/c
LOCUS       AX463127                 24 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 10 from Patent WO0250108.
ACCESSION   AX463127
VERSION     AX463127.1  GI:21886108
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Marchal,G., Pescher,P. and Romain,F.
  TITLE     Immunogenic glycopeptides, screening, preparation and uses
  JOURNAL   Patent: WO 0250108-A 10 27-JUN-2002;
            PASTEUR INSTITUT (FR)
FEATURES             Location/Qualifiers
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                     /note="linker"
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 GCTATGACGTTCCAAGG 18
          |||||||||||||||||
Db     21 GCTATGACGTTCCAAGG 5


RESULT 9
AR089858
LOCUS       AR089858                 37 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 140 from patent US 5994075.
ACCESSION   AR089858
VERSION     AR089858.1  GI:10016613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Goodfellow,P.N.
  TITLE     Methods for identifying a mutation in a gene of interest without a
            phenotypic guide
  JOURNAL   Patent: US 5994075-A 140 30-NOV-1999;
FEATURES             Location/Qualifiers
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Db      9 AGCTATGACCATCGAAGG 26


RESULT 10
AR167631
LOCUS       AR167631                 39 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 41 from patent US 6287763.
ACCESSION   AR167631
VERSION     AR167631.1  GI:17903423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Lee,F., Huszar,D. and Gu,W.
  TITLE     Screening methods for compounds useful in the regulation of body
            weight
  JOURNAL   Patent: US 6287763-A 41 11-SEP-2001;
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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LOCUS       AR151177                  48 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 3 from patent US 6232061.
ACCESSION   AR151177
VERSION     AR151177.1  GI:15117227
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Marchionni,M.Andrew. and Johnson,C.D.
  TITLE     Homology cloning
  JOURNAL   Patent: US 6232061-A 3 15-MAY-2001;
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RESULT 12
AX103935
LOCUS       AX103935                  19 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 127 from Patent WO0122972.
ACCESSION   AX103935
VERSION     AX103935.1  GI:13920132
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 127 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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Db       2 GCTATGTCGTTCCTAG 17


RESULT 13
AX131449/c
LOCUS       AX131449                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2667 from Patent WO0130362.
ACCESSION   AX131449
VERSION     AX131449.1  GI:14137754
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2667 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
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RESULT 14
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DEFINITION  Sequence 413 from Patent WO0197843.
ACCESSION   AX355385
VERSION     AX355385.1  GI:18620053
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 413 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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RESULT 15
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DEFINITION  Sequence 62 from patent US 6291173.
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ACCESSION AR169564
VERSION AR169564.1 GI:17907434
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Bartel,P.L. and Tavtigian,S.V.
TITLE MMSC2--an MMAC1 interacting protein
JOURNAL Patent: US 6291173-A 62 18-SEP-2001;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.3

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	19	AAV46003	Immune adjuvant AP
	2	20	100.0	20	21	AAZ48028	Immune remodeling
	3	20	100.0	20	24	AAL39184	Murine Toll-like r
	4	20	100.0	21	19	AAV44856	Probe for AP-1 gen
	5	20	100.0	21	19	AAV39812	AP1 sequence A. S
	6	20	100.0	21	20	AAX83976	AP1 sequence A. U
	7	20	100.0	21	20	AAV82453	AP1 comp oligonucl
	8	20	100.0	21	21	AAZ89651	Rabbit AP-1 bindin
	9	20	100.0	21	22	AAH26603	AP-1 oligonucleoti
	10	20	100.0	21	22	AAD13504	Rat AP-1 synthetic
	11	20	100.0	21	22	AAF87560	Consensus binding
	12	20	100.0	21	24	ABL56586	Oligonucleotide sp
	13	18.4	92.0	21	18	AAT85833	AP1 oligonucloide
	14	18.4	92.0	21	20	AAZ25683	Transcription fact
	15	18.4	92.0	21	20	AAX60221	Oligonucleotide AP
	16	18.4	92.0	21	20	AAX76049	cAMP response elem
	17	18.4	92.0	21	20	AAV08337	CRE element coding
	18	18.4	92.0	21	21	AAA52331	AP-1 footprinting
	19	18.4	92.0	21	22	AAI70580	Transcription fact
	20	18.4	92.0	21	22	AAD13506	Rat AP-1 synthetic
	21	18.4	92.0	21	22	AAF85085	Probe AP-1 used in
	22	18.4	92.0	21	24	ABK97978	Cell-TRAP method a
	23	18.4	92.0	21	24	ABK97979	Cell-TRAP method a
	24	18.4	92.0	21	24	ABK98231	Nucleic acid bindi
	25	18.4	92.0	21	24	ABK98232	Nucleic acid bindi
c	26	18.4	92.0	21	24	ABL60768	Nuclear factor-kap
	27	16.8	84.0	21	19	AAV44855	Probe for AP-1 gen
	28	16.8	84.0	21	22	AAH26605	AP-1 mutant oligon
	29	16.8	84.0	21	22	AAD13505	Rat AP-1 synthetic
	30	15.2	76.0	21	22	AAD13507	Rat AP-1 synthetic
	31	15.2	76.0	21	24	ABL60767	Nuclear factor-kap
	32	14.4	72.0	19	24	ABL44268	Human chromosome 1
	33	14.4	72.0	22	15	AAQ67303	Detection probe fo
	34	14.4	72.0	22	21	AAZ56897	AP-1 consensus seq
	35	14.4	72.0	25	22	AAF99633	Immunostimulatory
c	36	14.4	72.0	25	22	AAF99634	Immunostimulatory
c	37	14.4	72.0	25	24	ABL38910	Immunostimulatory
	38	14.4	72.0	25	24	ABL38913	Immunostimulatory
	39	14.4	72.0	60	24	ABN34717	Human spliced tran
c	40	14.2	71.0	60	24	ABN36654	Human spliced tran
	41	13.8	69.0	21	16	AAQ97424	Phage lambda (304-
	42	13.8	69.0	21	22	AAI70282	Phage lambda genom
	43	13.8	69.0	25	24	AAL42574	Phospholipase A1 p
	44	13.8	69.0	47	21	AAZ68783	Human map-related
c	45	13.8	69.0	60	22	AAF82009	1.0 kb DNA fragmen

ALIGNMENTS

RESULT 1
AAV46003
ID AAV46003 standard; DNA; 20 BP.
XX
AC AAV46003;
XX
DT 16-OCT-1998 (first entry)
XX
DE Immune adjuvant AP-1 #2.
XX
KW Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;
KW modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;
KW Ig class; autoimmune response; T-cell; B-cell; tumour; ss.
XX
OS Class Bacteria.
XX
PN EP855184-A1.
XX
PD 29-JUL-1998.
XX
PF 23-JAN-1997; 97EP-0101019.
XX
PR 23-JAN-1997; 97EP-0101019.
XX
PA (HEEG/) HEEG K.
PA (LIPF/) LIPFORD G B.
PA (WAGN/) WAGNER H.
XX
PI Heeg K, Lipford GB, Wagner H;
XX
DR WPI; 1998-389630/34.
XX

PT Antigenic composition comprises polynucleotide fragment and antigen
PT - used as vaccine to treat or prevent e.g. cancer or pathogen
PT infections and to modulate immune response e.g. tolerance break and
PT regulation of TH1/TH2 cells
XX
PS Example 5; Page 8; 28pp; English.
XX
CC AAV45993-V46019 are fragments of bacterial polynucleotides which are
CC used as immune adjuvants for inclusion into vaccines to treat cancer and
CC for prophylaxis and/or treatment of conditions caused by pathogenic
CC micro-organisms. The polynucleotide is used for modulation of an immune
CC response and the modulation is selected from the group break of
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig
CC classes, treatment of autoimmune responses and induction of tolerances.
CC DNA oligomers are used to enhance the reactivity of immune cells to
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination
CC against tumour-defined antigens and immunostimulatory substances in an
CC immune response against tumours and to suppress immune reactions of the
CC innate and acquired immune system. The composition is inexpensive and
CC stable and does not cause lethal shock, which happens with prior art
CC bacterial sequences.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGATGACTCAGCCGGAA 20
||||||||||||||||||||
Db 1 GCTTGATGACTCAGCCGGAA 20

RESULT 2
AAZ48028
ID AAZ48028 standard; DNA; 20 BP.
XX
AC AAZ48028;
XX
DT 08-MAR-2000 (first entry)
XX
DE Immune remodeling inducing CpG oligonucleotide control SEQ ID NO:108.
XX
KW Haematopoiesis; regulation; CpG oligonucleotide; phosphorothioate;
KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
KW immune response; allergic reaction; infectious disease; asthma;
KW thrombocytopaenia; immunohaemolytic disorder; genetic disorder;
KW haemoglobinopathy; kidney failure; chronic inflammatory disorder;
KW rheumatoid arthritis; ss.
XX
OS Synthetic.
XX
PN WO9958118-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99WO-IB01285.
XX
PR 14-MAY-1998; 98US-0085516.
PR 02-FEB-1999; 99US-0241653.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
PI Wagner H, Lipford G;
XX
DR WPI; 2000-062261/05.
XX
PT Use of CpG containing oligonucleotides for, e.g. inducing an
PT antigen-specific immune response -
XX
PS Example 1; Page 51; 116pp; English.
XX
CC The present invention describes a method using CpG containing
CC oligonucleotides (ONs) for regulating immune system remodeling and for
CC regulating haematopoiesis. The method for inducing an antigen-specific
CC immune response comprises: (1) administering an ON having a sequence
CC including at least the formula (I); and (2) exposing the subject to an
CC antigen at least 3 days after the ON is administered to the subject to
CC produce an antigen-specific immune response: 5' X1CGX2 3' (I), where
CC the ON = includes at least 8 nucleotides; C and G = unmethylated, and
CC X1 and X2 = nucleotides. The method can be used for inducing an immune
CC response against an antigen such as cells, cell extracts, proteins,
CC polysaccharides, polysaccharide conjugates, lipids, glycolipids,
CC carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
CC allergens. It can be used in a subject at risk of developing cancer or
CC an allergic reaction. It can also be used for treating an infectious
CC disease, allergic diseases and asthma, as well as thrombocytopaenia
CC which is drug-induced, due to an autoimmune disorder such as idiopathic
CC thrombocytopenic purpura, or resulting from accidental or therapeutic
CC radiation exposure. It can also be used for treating anaemia such as
CC drug-induced anaemia, immunohaemolytic disorder, genetic disorders such
CC as haemoglobinopathy and inherited haemolytic anaemia, inadequate
CC production despite adequate iron stores, chronic disease such as kidney
CC failure, and chronic inflammatory disorder such as rheumatoid arthritis,
CC or anaemia resulting from accidental or therapeutic radiation exposure.
CC AAZ47932 to AAZ48029 represent phosphorothioate CpG oligonucleotides
CC used in the exemplification of the present invention.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGATGACTCAGCCGGAA 20
||||||||||||||||||||
Db 1 GCTTGATGACTCAGCCGGAA 20

RESULT 3
AAL39184
ID AAL39184 standard; DNA; 20 BP.
XX
AC AAL39184;
XX
DT 05-SEP-2002 (first entry)
XX
DE Murine Toll-like receptor related CpG DNA SEQ ID No 59.
XX
KW Murine Toll-like receptor; TLR9; TLR7; TLR8; ISNA; ds.
XX
OS Unidentified.
XX
PN WO200222809-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US29229.
XX
PR 15-SEP-2000; 2000US-233035P.
PR 23-JAN-2001; 2001US-263657P.
PR 17-MAY-2001; 2001US-291726P.
PR 22-JUN-2001; 2001US-300210P.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Bauer S, Lipford G, Wagner H;
XX
DR WPI; 2002-393964/42.
XX
PT New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides,
PT useful for identifying species specificity of immunostimulatory nucleic
PT acid and identifying immunostimulatory nucleic acids -
XX

PS Disclosure; Page 76; 195pp; English.
XX
CC The invention relates to isolated murine Toll-like receptors (TLR)9,
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The
CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC TLR7, TLR8 and TLR9 polypeptides are also useful for comparing TLR9
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide
CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGATGACTCAGCCGGAA 20
||||||||||||||||||||
Db 1 GCTTGATGACTCAGCCGGAA 20

RESULT 4
AAV44856
ID AAV44856 standard; DNA; 21 BP.
XX
AC AAV44856;
XX
DT 21-OCT-1998 (first entry)
XX
DE Probe for AP-1 gene.
XX
KW Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
KW gene expression regulator; cellular stress; inflammatory response;
KW lymphocyte activity regulator; autoimmune response; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9825967-A1.
XX
PD 18-JUN-1998.
XX
PF 05-DEC-1997; 97WO-US22278.
XX
PR 12-DEC-1996; 96US-0032705.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Marsters SA;
XX
DR WPI; 1998-348457/30.
XX
PT Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in
PT assays for HVEM and to produce antibodies and transgenic animals,
PT e.g. for drug screening
XX
PS Example 3; Page 32; 46pp; English.
XX
CC This sequence is a probe for AP-1, used to determine if the
CC herpesvirus entry mediator (HVEM) protein of the invention activates
CC NF-kappaB. The HVEM protein is useful in quantitative diagnostic assays
CC for HVEM, in affinity purification of HVEM from recombinant cells/natural
CC sources and in competitive-type receptor binding assays. It can be used
CC to generate antibodies, also useful in diagnostic assays for HVEM and
CC affinity purification of HVEM. HVEM is believed to be a member of the
CC tumour necrosis factor receptor family. Transient transfection of HVEM
CC into human 293 cells caused marked activation of certain transcription
CC factors, suggesting that HVEM is involved in regulating gene expression
CC in response to infectious stimuli and cellular stress. The predominant
CC expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and
CC peripheral blood) suggests it may be a receptor in regulating lymphocyte
CC activity. Antibodies produced may be useful therapeutically, e.g.
CC antagonistic antibodies may be used to block excessive
CC inflammatory/autoimmune response resulting from e.g. AP-1 induction,
CC whilst agonistic antibodies may enhance HVEM regulation of such
CC induction. The DNA may be used diagnostically, e.g. to determine if DNA
CC and/or RNA encoding HVEM is present in cells, and to prepare HVEM
CC polypeptide recombinantly. It is also useful to produce non-human
CC transgenic animals (e.g. mice or rats), especially knockout animals
CC containing cells with an altered gene encoding HVEM polypeptide. Such
CC animals are useful in the development and screening of therapeutically
CC useful reagents.
XX
SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGATGACTCAGCCGGAA 20
||||||||||||||||||||
Db 2 GCTTGATGACTCAGCCGGAA 21

RESULT 5
AAV39812
ID AAV39812 standard; DNA; 21 BP.
XX
AC AAV39812;
XX
DT 24-SEP-1998 (first entry)
XX
DE AP1 sequence A.
XX
KW Mouse type 10 collagen promoter; AP1 sequence A; mutation; MEF-2;
KW identification; morphogen; OP-1; osteogenic protein 1; human c-fos; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826069-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US23211.
XX
PR 12-DEC-1996; 96US-0764522.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI Harada S, Rodan GA, Sampath KT;
XX
DR WPI; 1998-348526/30.
XX
PT Identifying morphogen analogues - by using DNA defining a
PT morphogen-responsive transcription activating element from a mouse
PT type X collagen promoter
XX
PS Claim 10; Page 61; 88pp; English.
XX
CC A method has been developed for identifying a compound that induces a
CC morphogen-mediated biological effect. The method comprises: (a) providing
CC a test cell comprising DNA defining a morphogen-responsive transcription
CC activating element (MRTAE), and, in operative association, a reporter

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CC   gene encoding a detectable gene product, the DNA, when present in a
CC   morphogen-responsive cell contacted with morphogen, serving to induce
CC   transcription of the reporter gene; (b) exposing the test cell to a
CC   candidate compound, and (c) detecting expression of the detectable gene
CC   product, the expression indicating the ability of the candidate compound
CC   to induce the morphogen-mediated biological effect. The present invention
CC   also describes: (1) a method for assessing whether a sample comprises a
CC   substance competent to bind to DNA; (2) a method for identifying a
CC   candidate compound that induces a morphogen-mediated biological effect;
CC   (3) a method for monitoring cell differentiation or tissue morphogenesis;
CC   and (4) a method for identifying a tissue responsive to a morphogen or
CC   analogue. The methods can be used for obtaining morphogen analogues. In
CC   particular they can be used for obtaining analogues of osteogenic protein
CC   1 (OP-1) for the treatment of a metabolic bone disease, e.g. a disease
CC   characterised by osteopenia. Analogues can also be obtained for treating
CC   mammals afflicted with ischemic, ulcerative or inflammatory tissue
CC   damage, or with injury or deterioration of a morphogen-responsive tissue
CC   such as bone, liver, kidney, nerve, gastrointestinal tract lining, tooth
CC   dentin or periodontal tissue. The present sequence represents AP1
CC   sequence A from the present invention.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 19;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 6
AAX83976
ID   AAX83976 standard; DNA; 21 BP.
XX
AC   AAX83976;
XX
DT   08-SEP-1999  (first entry)
XX
DE   AP1 sequence A.
XX
KW   Mouse; type 10 collage promoter; AP1 sequence A; osteogenic protein;
KW   OP-1; morphogen; bone morphogenic protein; BMP; soft tissue disorder;
KW   apoptosis; morphogen-activated regulatory pathway; tumour;
KW   cellular immune rejection; viral disease; ss.
XX
OS   Unidentified.
XX
PN   WO9931136-A2.
XX
PD   24-JUN-1999.
XX
PF   16-DEC-1998;   98WO-US26788.
XX
PR   01-DEC-1998;   98US-0110498.
PR   17-DEC-1997;   97US-0069931.
XX
PA   (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI   Cohen CM,  Kawabata M,  Miyazono K,  Oeda E,  Sampath KT;
XX
DR   WPI; 1999-418756/35.
XX
PT   Maintaining or restoring tissue-appropriate phenotype
XX
PS   Disclosure; Page 45; 50pp; English.
XX
CC   A method has been developed for maintaining or restoring tissue-
CC   appropriate phenotype by expression of a phenotype-specific protein or
CC   by inhibiting an intracellular pathway that induces expression of a
CC   gene that is an inhibitor of normal phenotype. The method is for
CC   restoring cellular phenotype in a cell effected by disease, damage or
CC   age. The method comprises activating an intracellular pathway that
CC   induces expression of a phenotype-specific gene. Another method is also
CC   described for restoring cellular phenotype in a cell effected by
CC   disease, damage or age, comprising inhibiting an intracellular pathway
CC   that induces expression of a gene (especially TGF-beta) that is an
CC   inhibitor of normal phenotype. The methods can be used to treat soft
CC   tissue disorders by affecting apoptosis by modulating a morphogen-
CC   activated regulatory pathway e.g. in tumours, cellular immune rejection
CC   and viral diseases. The present sequence is used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 7
AAV82453
ID   AAV82453 standard; DNA; 21 BP.
XX
AC   AAV82453;
XX
DT   12-APR-1999  (first entry)
XX
DE   AP1 comp oligonucleotide used in competition analysis.
XX
KW   Vascular endothelial growth factor; VEGF; human; hypoxia;
KW   vascular disease; tumour; cancer; angiogenesis; wound healing;
KW   therapy; diagnosis; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9856936-A1.
XX
PD   17-DEC-1998.
XX
PF   10-JUN-1998;   98WO-EP03517.
XX
PR   10-JUN-1997;   97EP-0109418.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Damert A,  Plate K,  Risau W;
XX
DR   WPI; 1999-080911/07.
XX
PT   New recombinant DNA - contains sequence that regulates
PT   hypoxia-induced expression, used for, e.g. treatment and diagnosis
PT   of vascular disease
XX
PS   Example 6; Page 41; 80pp; English.
XX
CC   Oligonucleotides hVEGF, hVEGF 5' DEL, AP1M1 and AP1M2 (see
CC   AAV82449-52), and competitor oligonucleotides AP1 comp, ATF comp
CC   and VL30 (see AAV82453-55) were used in electrophoretic mobility
CC   shift assays to determing which transcription factor(s) bind to
CC   the cis-acting element that is involved in the potentiation of
CC   hypoxia inducible factor 1 (HIF-1) mediated hypoxic induction
CC   of vascular endothelial growth factor (VEGF) gene regulatory
CC   sequences.  Experiments were performed using normoxic or hypoxic
CC   C6 cell nuclear extracts.  An AP1 consensus binding site was shown
CC   to compete for DNA-protein-complex formation at potentiating
CC   sequences.  The invention relates to recombinant DNA molecules
CC   comprising regulatory sequences of the VEGF gene, especially the
CC   3' untranslated region (see AAV82439) and promoter (see AAV82440),
CC   being capable of modulating hypoxia inducible expression of a
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CC   heterologous DNA in vivo.  Such recombinant DNA molecules, vectors,
CC   host cells and transgenic animals can be used to identify and
CC   develop compounds and methods for diagnosing, treating, preventing
CC   and/or delaying a vascular or tumour disease.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 8
AAZ89651
ID   AAZ89651 standard; DNA; 21 BP.
XX
AC   AAZ89651;
XX
DT   28-JUN-2000  (first entry)
XX
DE   Rabbit AP-1 binding site consensus DNA sequence.
XX
KW   Transcription factor; AP-1; C/EBP; CCAAT/enhancer binding protein;
KW   cardiant; gene therapy; coronary angioplasty; stent implantation;
KW   ET-1 gene; smooth muscle cell; aorta carotis; treatment; rabbit;
KW   coronary heart disease; ds.
XX
OS   Oryctolagus cuniculus.
XX
PN   DE29916160-U1.
XX
PD   09-MAR-2000.
XX
PF   31-AUG-1999;   99WO-US20047.
XX
PR   25-MAY-1999;   99DE-1023892.
XX
PA   (CARD-) CARDIOGENE GENTHERAPEUTISCHE SYSTEME AG.
XX
DR   WPI; 2000-247751/22.
XX
PT   Double stranded oligonucleotides targeting genes encoding AP-1, C/EBP
PT   and related transcription factors useful for treatment of coronary
PT   heart disease  -
XX
PS   Example 6; Page 37; 53pp; German.
XX
CC   This invention describes novel double stranded nucleic acids, which bind
CC   specifically to transcription factors AP-1, C/EBP (CCAAT/Enhancer
CC   Binding Protein) or related transcription factors. The products of the
CC   invention have cardiant activity and are used in gene therapy. Patients
CC   who have had coronary angioplasty or stent implantation may be at risk
CC   from an increased expression of certain genes due to the physical weight
CC   of the devices used inducing a number of genes involved in the cell
CC   cycle. The AP-1 and C/EBP specific double stranded nucleic acids can be
CC   used to block activation of the ET-1 gene in smooth muscle cells of the
CC   aorta carotis. The nucleic acids are therefore useful in treatment of
CC   coronary heart diseases. This sequence represents a consensus AP-1
CC   binding site isolated from rabbit (Oryctolagus cuniculus) which is used
CC   to illustrate the method of the invention.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 21;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 9
AAH26603
ID   AAH26603 standard; DNA; 21 BP.
XX
AC   AAH26603;
XX
DT   12-NOV-2001  (first entry)
XX
DE   AP-1 oligonucleotide.
XX
KW   Melanoma differentiation associated gene-7; Mda-7; human;
KW   promoter; neuroblastoma; astrocytoma; glioblastoma multiforme;
KW   cervical cancer; breast cancer; colon cancer; prostate cancer;
KW   osteosarcoma; chondrosarcoma; tumour; therapy; PCR primer;
KW   electrophoretic mobility shift assay; EMSA; AP-1;
KW   transcription factor; ss.
XX
OS   Homo sapiens.
XX
PN   WO200164921-A1.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06782.
XX
PR   29-FEB-2000; 2000US-0515369.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Fisher PB,  Madireddi MT;
XX
DR   WPI; 2001-565508/63.
XX
PT   Melanoma differentiation associated gene-7 promoter capable of
PT   treating cancer comprises directing transcription of heterologous
PT   coding sequence encoding tumour suppressor polypeptide positioned
PT   downstream, useful for treating cancer  -
XX
PS   Example 2; Page 70; 132pp; English.
XX
CC   The present sequence is that of an AP-1 transcription factor
CC   oligonucleotide.  This was used in electrophoretic mobility
CC   shift assays (EMSA) to examine transcription factor binding to
CC   the human melanoma differentiation associated gene-7 (mda-7)
CC   promoter (see AAH26595).  Results demonstrated that cJUN/AP-1 and
CC   C/EBP-beta transcription factors bind to defined sites within the
CC   mda-7 promoter during the process of terminal differentiation in
CC   human melanoma cells.  The invention provides recombinant
CC   expression constructs in which the mda-7 promoter is operably
CC   linked to a coding sequence encoding a tumour suppressor protein.
CC   A pharmaceutical composition including the recombinant expression
CC   construct is used in a claimed method of treating melanoma,
CC   neuroblastoma, astrocytoma, glioblastoma multiforme, cervical
CC   cancer, breast cancer, colon cancer, prostate cancer, osteosarcoma,
CC   chondrosarcoma or a cancer of the central nervous system.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 10
AAD13504
ID   AAD13504 standard; DNA; 21 BP.
```

```
XX
AC   AAD13504;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Rat AP-1 synthetic duplex probe #1.
XX
KW   Antioxidative enzyme; catalase; CAT; superoxide dismutase; SOD; therapy;
KW   reactive oxygen species; ROS; free radical; dietary supplement; stroke;
KW   AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;
KW   myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;
KW   trauma; premature aging; neurodegenerative disease; Tardive dyskinesia;
KW   Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;
KW   arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;
KW   senility; Down's syndrome; macular degeneration; septic shock; epilepsy;
KW   polytraumatous shock; schizophrenia; antiulcer; clozapine; tranquilliser;
KW   cardiant; cerebroprotective; vulnerary; nootropic; Huntington's disease;
KW   anticonvulsant; neuroprotective; antiarthritic; antiinflammatory; burn;
KW   cytostatic; leukaemia; ophthalmological; antibacterial; probe; ds.
XX
OS   Rattus sp.
XX
PN   WO200136454-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US31764.
XX
PR   18-NOV-1999;   99US-0166381.
XX
PA   (CERE-) CEREMEDIX INC.
XX
PI   Shashoua VE;
XX
DR   WPI; 2001-496512/54.
XX
PT   Novel peptide compound that up regulates expression of a gene encoding
PT   antioxidative enzymes, used to treat or prevent conditions caused by
PT   undesirable elevation of reactive oxygen species and other free
PT   radicals -
XX
PS   Example 3; Page 50; 102pp; English.
XX
CC   The invention relates to peptide compounds and methods for upregulating
CC   expression of a gene encoding an antioxidative enzyme, such as catalase
CC   (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative
CC   effects of reactive oxygen species (ROS) and other free radicals. The
CC   peptides are used as components of pharmaceuticals and dietary
CC   supplements. The peptides are used to treat or to prevent diseases and
CC   conditions characterised by undesirable elevation of ROS and other free
CC   radicals, to upregulate AP-1 transcription factor gene expression and to
CC   treat pain. The disease or conditions include renal reperfusion damage,
CC   cerebral ischaemia (stroke), myocardial infarction (heart attack), head
CC   trauma, atherosclerosis, brain trauma, oxygen toxicity in premature
CC   infants, premature aging, spinal cord trauma, neurodegenerative diseases,
CC   Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC   Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,
CC   ulcerative colitis, human leukaemia and other cancers characterised by
CC   elevation of ROS or free radicals, age-related elevation of ROS or free
CC   radicals, senility, Down's syndrome, macular degeneration, cataracts,
CC   septic shock, polytraumatous shock, schizophrenia, burn injuries,
CC   epilepsy, radiation and/or drug-induced elevation of ROS and free
CC   radicals, where the drug is a neuroleptic or a drug such as clozapine
CC   defined in the specification and Tardive dyskinesia. The present
CC   sequence is a duplex probe used to assay rat AP-1 transcription
CC   factor activation.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match           100.0%;  Score 20;  DB 22;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 11
AAF87560
ID   AAF87560 standard; DNA; 21 BP.
XX
AC   AAF87560;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Consensus binding site for AP-1.
XX
KW   Transcription modulation; AP-1; C/EBP; vascular; coronary; myocardial;
KW   CCAT/enhancer binding protein; ds.
XX
OS   Unidentified.
XX
PN   CA2300328-A1.
XX
PD   14-MAR-2001.
XX
PF   13-MAR-2000; 2000CA-2300328.
XX
PR   14-SEP-1999;   99JP-0261035.
PR   14-SEP-1999;   99DE-2016160.
XX
PA   (CARD-) CARDIOGENE GENTHERAP SYSTEME AG.
XX
PI   Hecker M,  Lauth M,  Wagner AH;
XX
DR   WPI; 2001-316865/34.
XX
PT   Modulating gene transcription in an endothelial, vascular or cardiac
PT   cell, useful for treating vascular proliferative diseases, comprises
PT   contacting the cell with a nucleic acid capable of sequence-specific
PT   binding to AP-1 or C/EBP  -
XX
PS   Claim 27; Page 36; 57pp; English.
XX
CC   The present invention relates to modulating the transcription of
CC   at least one gene in an endothelial, vascular or cardiac cell
CC   by contacting the cell with a composition of one or more double
CC   stranded nucleic acids capable of sequence-specific binding to
CC   the transcription factor AP-1 or C/EBP (CCAT/enhancer binding
CC   protein). The method is also useful for treating vascular
CC   diseases, specifically vascular proliferative disorders,
CC   coronary heart diseases and myocardial infarction. The present
CC   sequence is the consensus binding site for AP-1.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match           100.0%;  Score 20;  DB 22;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||||||||||||||
Db       2 GCTTGATGACTCAGCCGGAA 21


RESULT 12
ABL56586
ID   ABL56586 standard; DNA; 21 BP.
XX
AC   ABL56586;
XX
DT   30-JUL-2002  (first entry)
XX
DE   Oligonucleotide specific for nuclear transcription factor AP-1.
XX
```

```
KW   Nuclear transcription factor AP-1; R-flurbiprofen; S-flurbiprofen;
KW   R-Arylpropionic acid; joint destruction; antirheumatic;
KW   rheumatic disease; ss.
XX
OS   Synthetic.
XX
PN   WO200224190-A1.
XX
PD   28-MAR-2002.
XX
PF   24-SEP-2001; 2001WO-EP11004.
XX
PR   25-SEP-2000; 2000DE-1047319.
XX
PA   (PAZA-) PAZ ARZNEIMITTEL ENTWICKLUNGS GMBH.
XX
PI   Geisslinger G,  Groesch S;
XX
DR   WPI; 2002-401951/43.
XX
PT   Use of R-arylpropionic acids in the production of medicaments, useful
PT   for the treatment of illnesses, e.g. rheumatic diseases, influenced by
PT   activation of nuclear transcription factor -
XX
PS   Example; Page 10; 20pp; German.
XX
CC   The present sequence represents an oligonucleotide specific for nuclear
CC   transcription factor AP-1. The oligonucleotide was used to demonstrate
CC   that while R-flurbiprofen inhibited AP-1 DNA binding in a
CC   dosage-dependent manner (binding was completely suppressed at 1000
CC   microgram), S-flurbiprofen reduced AP-1 DNA binding at only 1000
CC   microgram. The specification describes the use of R-Arylpropionic acids
CC   or their salts or derivatives in the production of medicaments which
CC   inhibit the activation of nuclear transcription factor AP-1 and are
CC   useful for the treatment of illnesses which are influenced by this
CC   factor. The R-arylpropionic acids arrest joint destruction but do not
CC   have the severe side effects associated with standard therapy using
CC   long-term antirheumatics. The medicaments are used in the treatment of
CC   rheumatic diseases, preferably in combination with basic therapeutics.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 24;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          ||||||||||||||||||||
Db      2 GCTTGATGACTCAGCCGGAA 21


RESULT 13
AAT85833
ID   AAT85833 standard; DNA; 21 BP.
XX
AC   AAT85833;
XX
DT   21-NOV-1997  (first entry)
XX
DE   AP1 oligonucloide used in gel shift assay.
XX
KW   Activating transcription factor 1; ATF1; CREB; recognition sequence;
KW   cyclic AMP responsive element binding protein; inhibition; binding;
KW   proliferation; virus; cancer; HTLV1; leukaemia; antibody; ss.
XX
OS   Synthetic.
XX
PN   US5641486-A.
XX
PD   24-JUN-1997.
XX
PF   18-MAR-1994;   94US-0210880.
XX
PR   18-MAR-1994;   94US-0210880.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Hinrichs SH,  Orten DJ;
XX
DR   WPI; 1997-340900/31.
XX
PT   Inhibiting replication of cancer cells or viruses - with inhibitor
PT   that binds to peptide sequence of activating transcription factor 1
XX
PS   Example 2; Column 6; 17pp; English.
XX
CC   This oligonucleotide sequence corresponds to the ecognition sequence AP1
CC   to which members of the activating transcription factor 1 (ATF1)-cyclic
CC   AMP responsive element binding protein (CREB) family of proteins bind.
CC   The sequence was used in a gel shift mobility assay to identify agents
CC   which inhibit the binding of ATF1 to its recognition sequence.  The
CC   agents are preferably antibodies, small molecules or polypeptides,
CC   especially the complementarity determining region of monoclonal antibody
CC   MAb4.  The agents cause inhibition of transcription by dissociating ATF1
CC   from its target gene and thus will prevent proliferation of e.g. a virus
CC   or cancer cell, such as HTLV1-mediated leukaemic cell proliferation.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;

  Query Match             92.0%;  Score 18.4;  DB 18;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 3.1;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          |||||||| ||||||||||
Db      2 GCTTGATGAGTCAGCCGGAA 21


RESULT 14
AAZ25683
ID   AAZ25683 standard; DNA; 21 BP.
XX
AC   AAZ25683;
XX
DT   06-JAN-2000  (first entry)
XX
DE   Transcription factor AP-1 (c-jun) oligonucleotide.
XX
KW   Neuroprotective; calcium binding; stroke; neurodegenerative disease;
KW   blood-brain barrier; cerebral ischaemia; Alzheimer's disease;
KW   memory deficit; aging; ss.
XX
OS   Synthetic.
XX
PN   WO9940112-A1.
XX
PD   12-AUG-1999.
XX
PF   28-JAN-1999;   99WO-US01786.
XX
PR   10-FEB-1998;   98US-0021247.
XX
PA   (NEUR-) NEUROMEDICA INC.
XX
PI   Shashoua VE;
XX
DR   WPI; 1999-610582/52.
XX
PT   Neuroprotective peptides, which bind calcium, are useful for treating
PT   stroke and other neurodegenerative diseases  -
XX
PS   Example 4; Page 31; 65pp; English.
XX
CC   The present invention describes a composition comprising an isolated
CC   peptide, which comprises the amino acid sequence (I) or (Ia):
CC   X1-XX3-XX5-XX7-XX9-XXX12 (I); X5-X6-X7-X8-X9-X10-X11-X12 (Ia); where
```

CC X1 = Asp, Gln, Gly or Tyr; X = any amino acid; X3 = Asp, Asn, Thr or Glu;
CC X5 = Asp, Ser, Gly, Asn or Leu; X7 = Ala, Asp, Phe, Lys, Thr, Tyr, Arg,
CC Val, Cys or Ser; X9 = Asp, Glu, Gly, Seer, Thr, Met or Asn; and X12 =
CC Glu, Gln, Ala, Leu or Asn. (I) and (Ia) are neuroprotective calcium
CC binding peptides. (I) is used to treat a condition characterized by
CC cerebral ischaemia. (I) reduces the neurotoxic effect of cerebral
CC ischaemia. (I) is used to increase neuronal cell AP-1 or NF-IL6
CC transcription factor activity. The peptides are also useful for binding
CC calcium. The peptide can be conjugated with a compound which facilitates
CC transport across the blood brain barrier into the brain or it can be
CC administered with a compound that increases transport across the blood
CC brain barrier. Molecules that protect neurons against the ischaemic
CC effects of stroke will also be useful for treating Alzheimer's disease,
CC as well as the memory deficits that are characteristic of the aging
CC process. The present sequence represents an oligonucleotide used in
CC the exemplification of the present invention.
XX
SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;

Query Match 92.0%; Score 18.4; DB 20; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.1;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTGATGACTCAGCCGGAA 20
||||||||| ||||||||||
Db 2 GCTTGATGAGTCAGCCGGAA 21

RESULT 15
AAX60221
ID AAX60221 standard; DNA; 21 BP.
XX
AC AAX60221;
XX
DT 11-AUG-1999 (first entry)
XX
DE Oligonucleotide AP-1.
XX
KW keratin K1 based expression vector; epidermal cell expression;
KW mammalian K1 keratin gene; primer; ss.
XX
OS Synthetic.
XX
PN US5914265-A.
XX
PD 22-JUN-1999.
XX
PF 01-NOV-1993; 93US-0147777.
XX
PR 01-NOV-1993; 93US-0147777.
PR 30-APR-1992; 92US-0876289.
PR 29-OCT-1993; 93US-0145387.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Greenhalgh DA, Roop DR, Rothnagel JA, Yuspa SH;
XX
DR WPI; 1999-370501/31.
XX
PT Keratin K1 expression vectors
XX
PS Example 16; Column 35; 50pp; English.
XX
CC The specification describes a keratin K1 based expression vector, which
CC does not comprise a K1 keratin encoding gene sequence, for expression
CC in an epidermal cell. The vector comprises a 5' flanking region from a
CC mammalian gene including the necessary sequences for expression, a
CC 3' flanking region from a mammalian K1 keratin gene which regulates
CC expression in an epidermal cell, and a linker connecting the 5' flanking
CC region to the nucleic acid sequence, where the linker has a position
CC for inserting the nucleic acid sequence but lacks the coding sequence
CC of a gene with which it is naturally associated. The genetic material
CC comprising the vector may encode a hormone, a receptor, a growth factor,
CC an enzyme, a drug, a tumour suppressor, an apolipoprotein, a clotting
CC factor, an antigen, an oncogene or a transforming gene. The present
CC oligonucleotide was used in the course of the invention.
XX
SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;

Query Match 92.0%; Score 18.4; DB 20; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.1;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTGATGACTCAGCCGGAA 20
||||||||| ||||||||||
Db 2 GCTTGATGAGTCAGCCGGAA 21

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Job time : 105.319 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
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Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

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Maximum Match 100%
Listing first 45 summaries

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35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89791	A89791 Sequence 13
2		20	100.0	20	6	A90878	A90878 Sequence 13
3		20	100.0	20	6	AX023404	AX023404 Sequence
4		20	100.0	20	6	AX455627	AX455627 Sequence
5		20	100.0	22	6	AR060640	AR060640 Sequence
6		20	100.0	22	6	AR070792	AR070792 Sequence
7		20	100.0	22	6	AX195274	AX195274 Sequence
8		20	100.0	48	6	AX377574	AX377574 Sequence
9	c	20	100.0	48	6	AX377574	AX377574 Sequence
10		20	100.0	49	6	AX127457	AX127457 Sequence
11	c	20	100.0	49	6	AX127457	AX127457 Sequence
12		20	100.0	49	6	AX127459	AX127459 Sequence
13	c	20	100.0	49	6	AX127459	AX127459 Sequence
14		20	100.0	49	6	AX377573	AX377573 Sequence
15		19	95.0	21	6	AX104633	AX104633 Sequence
16	c	19	95.0	21	6	AX104634	AX104634 Sequence
17		19	95.0	21	6	AX355087	AX355087 Sequence
18	c	19	95.0	21	6	AX355201	AX355201 Sequence
19		19	95.0	46	6	I72381	I72381 Sequence 12
20		19	95.0	46	6	I72382	I72382 Sequence 13
21		18.4	92.0	22	6	E07877	E07877 Synthetic n
22	c	18	90.0	46	6	I72381	I72381 Sequence 12
23	c	18	90.0	46	6	I72382	I72382 Sequence 13
24	c	16.8	84.0	49	6	AX377573	AX377573 Sequence
25	c	15.8	79.0	31	6	AR091898	AR091898 Sequence
26	c	15.8	79.0	31	6	E64477	E64477 Sugar-respo
27	c	15.8	79.0	31	6	I77207	I77207 Sequence 4
28	c	15.8	79.0	66	6	AX207285	AX207285 Sequence
29	c	15.2	76.0	80	6	AX002555	AX002555 Sequence
30	c	15.2	76.0	80	6	E27453	E27453 cdc25B Gene
31	c	14.8	74.0	27	6	AX182197	AX182197 Sequence
32	c	14.8	74.0	27	6	AX382003	AX382003 Sequence
33	c	14.4	72.0	58	6	AR034640	AR034640 Sequence
34	c	14.4	72.0	58	6	I70120	I70120 Sequence 26
35		14.4	72.0	60	6	AR034639	AR034639 Sequence
36		14.4	72.0	60	6	I70119	I70119 Sequence 25
37		13.6	68.0	33	6	AX363257	AX363257 Sequence
38	c	13.6	68.0	59	9	HSGROUCH1	U88831 Human grouc
39	c	13.6	68.0	65	6	AR121168	AR121168 Sequence
40	c	13.6	68.0	65	6	BD003583	BD003583 Methods a
41	c	13.4	67.0	87	9	AF188738S5	AF188742 Homo sapi
42	c	13.2	66.0	39	6	AX006290	AX006290 Sequence
43		13.2	66.0	51	6	AX204497	AX204497 Sequence
44		13.2	66.0	81	14	AF221250	AF221250 Hepatitis
45		13.2	66.0	81	14	AF221252	AF221252 Hepatitis

ALIGNMENTS

RESULT 1
A89791
LOCUS A89791 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 13 from Patent WO9832462.
ACCESSION A89791
VERSION A89791.1 GI:6738305
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 13 30-JUL-1998;

LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES Location/Qualifiers
source 1. .20
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2 a 5 c 11 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGATCGGGGCGGGGCGAGC 20
||||||||||||||||||||
Db 1 TCGATCGGGGCGGGGCGAGC 20

RESULT 2
A90878
LOCUS A90878 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 13 from Patent EP0855184.
ACCESSION A90878
VERSION A90878.1 GI:6739281
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Heeg,K.P. and Lipford,G.B.
TITLE Pharmaceutical composition comprising a polynucleotide and an antigen especially for vaccination
JOURNAL Patent: EP 0855184-A 13 29-JUL-1998;
HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2 a 5 c 11 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGATCGGGGCGGGGCGAGC 20
||||||||||||||||||||
Db 1 TCGATCGGGGCGGGGCGAGC 20

RESULT 3
AX023404
LOCUS AX023404 20 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 19 from Patent WO0014217.
ACCESSION AX023404
VERSION AX023404.1 GI:10183804
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.
TITLE G-motif oligonucleotides and uses thereof
JOURNAL Patent: WO 0014217-A 19 16-MAR-2000;
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic, no natural origin"
BASE COUNT 2 a 5 c 11 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGATCGGGGCGGGGCGAGC 20
||||||||||||||||||||
Db 1 TCGATCGGGGCGGGGCGAGC 20

RESULT 4
AX455627
LOCUS AX455627 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 104 from Patent WO0222809.
ACCESSION AX455627
VERSION AX455627.1 GI:21714695
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bauer,S., Lipford,G. and Wagner,H.
TITLE Process for high throughput screening of cpg-based immuno-agonist/antagonist
JOURNAL Patent: WO 0222809-A 104 21-MAR-2002;
Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
BASE COUNT 2 a 5 c 11 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGATCGGGGCGGGGCGAGC 20
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Db 1 TCGATCGGGGCGGGGCGAGC 20

RESULT 5
AR060640
LOCUS AR060640 22 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5840832.
ACCESSION AR060640
VERSION AR060640.1 GI:5987090
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ono,S.Jeremy. and Strominger,J.L.
TITLE Transcription factor regulating MHC expression, CDNA and genomic clones encoding same and retroviral expression constructs thereof
JOURNAL Patent: US 5840832-A 12 24-NOV-1998;
FEATURES Location/Qualifiers
source 1. .22
/organism="unknown"
BASE COUNT 3 a 5 c 11 g 3 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGATCGGGGCGGGGCGAGC 20
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Db 3 TCGATCGGGGCGGGGCGAGC 22

RESULT 6

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AR070792
LOCUS       AR070792                22 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 12 from patent US 5908762.
ACCESSION   AR070792
VERSION     AR070792.1  GI:7221680
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Ono,S.Jeremy. and Strominger,J.L.
  TITLE     Transcription factor regulating MHC expression CDNA and genomic
            clones encoding same and retroviral expression constructs thereof
  JOURNAL   Patent: US 5908762-A 12 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        3 a      5 c     11 g      3 t
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
          ||||||||||||||||||||
Db      3 TCGATCGGGGCGGGGCGAGC 22


RESULT 7
AX195274
LOCUS       AX195274                22 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 10 from Patent WO0151671.
ACCESSION   AX195274
VERSION     AX195274.1  GI:15385825
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Mccarthy,J. and Cordell,B.
  TITLE     Methods for identifying inhibitors of neuronal degeneration
  JOURNAL   Patent: WO 0151671-A 10 19-JUL-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide"
BASE COUNT        3 a      5 c     11 g      3 t
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
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Db      3 TCGATCGGGGCGGGGCGAGC 22


RESULT 8
AX377574
LOCUS       AX377574                48 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 51 from Patent WO0212553.
ACCESSION   AX377574
VERSION     AX377574.1  GI:19573760
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdorf,H. and
            Muth,J.
  TITLE     Method for detecting mutations in nucleotide sequences
  JOURNAL   Patent: WO 0212553-A 51 14-FEB-2002;
            Nanogen Recognomics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen Sequenz:
                     Hairpin-Oligonucleotid"
BASE COUNT        6 a     16 c     16 g     10 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
          ||||||||||||||||||||
Db      3 TCGATCGGGGCGGGGCGAGC 22


RESULT 9
AX377574/c
LOCUS       AX377574                48 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 51 from Patent WO0212553.
ACCESSION   AX377574
VERSION     AX377574.1  GI:19573760
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdorf,H. and
            Muth,J.
  TITLE     Method for detecting mutations in nucleotide sequences
  JOURNAL   Patent: WO 0212553-A 51 14-FEB-2002;
            Nanogen Recognomics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen Sequenz:
                     Hairpin-Oligonucleotid"
BASE COUNT        6 a     16 c     16 g     10 t
ORIGIN

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Qy      1 TCGATCGGGGCGGGGCGAGC 20
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Db     46 TCGATCGGGGCGGGGCGAGC 27


RESULT 10
AX127457
LOCUS       AX127457                49 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1 from Patent WO0131057.
ACCESSION   AX127457
VERSION     AX127457.1  GI:14134020
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Muth,J. and Windhab,N.
  TITLE     Double-strand nucleic acid probes and the use thereof
  JOURNAL   Patent: WO 0131057-A 1 03-MAY-2001;
            Aventis Research & Technologies GmbH & Co KG (DE)
FEATURES             Location/Qualifiers
     source          1. .49
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Detektorsequenz mit einem Amino-Modifier
                     dT-Baustein an Position 25"
BASE COUNT        6 a     16 c     16 g     11 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
          ||||||||||||||||||||
Db      3 TCGATCGGGGCGGGGCGAGC 22


RESULT 11
AX127457/c
LOCUS       AX127457                 49 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1 from Patent WO0131057.
ACCESSION   AX127457
VERSION     AX127457.1  GI:14134020
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Muth,J. and Windhab,N.
  TITLE     Double-strand nucleic acid probes and the use thereof
  JOURNAL   Patent: WO 0131057-A 1 03-MAY-2001;
            Aventis Research & Technologies GmbH & Co KG (DE)
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Detektorsequenz mit einem Amino-Modifier
                     dT-Baustein an Position 25"
BASE COUNT        6 a     16 c     16 g     11 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
          ||||||||||||||||||||
Db     47 TCGATCGGGGCGGGGCGAGC 28


RESULT 12
AX127459
LOCUS       AX127459                 49 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3 from Patent WO0131057.
ACCESSION   AX127459
VERSION     AX127459.1  GI:14134028
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Muth,J. and Windhab,N.
  TITLE     Double-strand nucleic acid probes and the use thereof
  JOURNAL   Patent: WO 0131057-A 3 03-MAY-2001;
            Aventis Research & Technologies GmbH & Co KG (DE)
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Detektorsequenz mit einem Amino-Modifier
                     dT-Baustein an Position 27"
BASE COUNT        6 a     16 c     16 g     11 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
          ||||||||||||||||||||
Db      3 TCGATCGGGGCGGGGCGAGC 22


RESULT 13
AX127459/c
LOCUS       AX127459                 49 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3 from Patent WO0131057.
ACCESSION   AX127459
VERSION     AX127459.1  GI:14134028
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Muth,J. and Windhab,N.
  TITLE     Double-strand nucleic acid probes and the use thereof
  JOURNAL   Patent: WO 0131057-A 3 03-MAY-2001;
            Aventis Research & Technologies GmbH & Co KG (DE)
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Detektorsequenz mit einem Amino-Modifier
                     dT-Baustein an Position 27"
BASE COUNT        6 a     16 c     16 g     11 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAGC 20
          ||||||||||||||||||||
Db     47 TCGATCGGGGCGGGGCGAGC 28


RESULT 14
AX377573
LOCUS       AX377573                 49 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 50 from Patent WO0212553.
ACCESSION   AX377573
VERSION     AX377573.1  GI:19573759
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdorf,H. and
            Muth,J.
  TITLE     Method for detecting mutations in nucleotide sequences
  JOURNAL   Patent: WO 0212553-A 50 14-FEB-2002;
            Nanogen Recognomics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen Sequenz:
                     Hairpin-Oligonucleotid"
BASE COUNT        6 a     14 c     16 g     13 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3e+02;
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Qy      1 TCGATCGGGGCGGGGCGAGC 20
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Db      3 TCGATCGGGGCGGGGCGAGC 22


RESULT 15
AX104633
LOCUS       AX104633                21 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 825 from Patent WO0122972.
ACCESSION   AX104633
VERSION     AX104633.1  GI:13920830
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 825 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 8.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGATCGGGGCGGGGCGAG 19
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Db      3 TCGATCGGGGCGGGGCGAG 21


Search completed: December 12, 2002, 02:55:46
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:05:40 ; Search time 22.2464 Seconds
(without alignments)
275.709 Million cell updates/sec

Title: US-09-355-254F-11
Perfect score: 20
Sequence: 1 gcttgatgactcagccggaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	20	100.0	21	2	US-08-507-750-2	Sequence 2, Appli
	3	20	100.0	21	3	US-08-764-522A-2	Sequence 2, Appli
	4	20	100.0	21	3	US-08-764-528-2	Sequence 2, Appli
	5	20	100.0	21	3	US-08-872-859-2	Sequence 2, Appli
	6	18.4	92.0	21	1	US-08-283-591-15	Sequence 15, Appl
	7	18.4	92.0	21	1	US-08-210-880B-3	Sequence 3, Appli
c	8	18.4	92.0	21	2	US-08-632-275-1	Sequence 1, Appli
	9	18.4	92.0	21	2	US-08-771-411-3	Sequence 3, Appli
c	10	18.4	92.0	21	3	US-09-097-929-1	Sequence 1, Appli
	11	18.4	92.0	21	4	US-09-021-247-8	Sequence 8, Appli
	12	18.4	92.0	21	4	US-08-088-661F-8	Sequence 8, Appli
	13	18.4	92.0	21	4	US-08-088-661F-42	Sequence 42, Appl
	14	13.8	69.0	21	1	US-08-203-198-1	Sequence 1, Appli
c	15	13.6	68.0	26	1	US-07-791-213D-68	Sequence 68, Appl
c	16	13.6	68.0	26	1	US-08-293-150A-68	Sequence 68, Appl
c	17	13.4	67.0	41	2	US-08-818-604-8	Sequence 8, Appli
c	18	12.8	64.0	18	3	US-09-289-377-17	Sequence 17, Appl
c	19	12.8	64.0	22	1	US-08-339-152A-7	Sequence 7, Appli
	20	12.8	64.0	27	4	US-09-564-805-204	Sequence 204, App
c	21	12.8	64.0	44	1	US-08-458-084-17	Sequence 17, Appl
c	22	12.8	64.0	44	1	US-08-205-508-17	Sequence 17, Appl
c	23	12.8	64.0	44	5	PCT-US95-02945-17	Sequence 17, Appl
c	24	12.6	63.0	20	4	US-09-326-186B-171	Sequence 171, App
	25	12.6	63.0	30	3	US-08-913-842-52	Sequence 52, Appl
	26	12.6	63.0	38	4	US-08-341-560B-18	Sequence 18, Appl
	27	12.6	63.0	38	4	US-09-139-802-207	Sequence 207, App
	28	12.6	63.0	38	4	US-09-425-638A-3	Sequence 3, Appli
	29	12.6	63.0	38	4	US-09-543-004-3	Sequence 3, Appli
	30	12.4	62.0	23	2	US-08-350-260A-573	Sequence 573, App
	31	12.4	62.0	37	1	US-08-203-534-2	Sequence 2, Appli
	32	12.4	62.0	41	2	US-08-350-260A-586	Sequence 586, App
	33	12.2	61.0	20	1	US-08-129-719-13	Sequence 13, Appl
	34	12.2	61.0	20	1	US-08-306-871-13	Sequence 13, Appl
	35	12.2	61.0	20	1	US-08-569-959-13	Sequence 13, Appl
	36	12.2	61.0	20	2	US-08-229-528-37	Sequence 37, Appl
	37	12.2	61.0	20	3	US-09-429-323-77	Sequence 77, Appl
c	38	12.2	61.0	35	1	US-08-310-356-31	Sequence 31, Appl
c	39	12.2	61.0	35	1	US-08-310-356-35	Sequence 35, Appl
c	40	12.2	61.0	44	4	US-09-110-959A-11	Sequence 11, Appl
	41	12.2	61.0	48	4	US-09-025-769B-94	Sequence 94, Appl
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	43	12	60.0	34	2	US-08-577-492-16	Sequence 16, Appl
	44	12	60.0	34	4	US-09-079-630-16	Sequence 16, Appl
	45	12	60.0	66	2	US-08-652-816A-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-08-507-598-2
; Sequence 2, Application US/08507598
; Patent No. 5834188
; GENERAL INFORMATION:
; APPLICANT: HARADA, SHUN-ICHI
; APPLICANT: SAMPATH, T. K.
; APPLICANT: RODAN, GIDEON A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,598
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..21
; OTHER INFORMATION: /product= "AP1 SEQUENCE"
US-08-507-598-2

Query Match 100.0%; Score 20; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.058;

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RESULT 2
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; Sequence 2, Application US/08507750
; Patent No. 5932716
;  GENERAL INFORMATION:
;    APPLICANT:  SAMPATH, T. K.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR IDENTIFYING
;    TITLE OF INVENTION:  MORPHOGEN ANALOGS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, TESTA, HURWITZ &
;      ADDRESSEE:  THIBEAULT
;      STREET:  53 STATE STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/507,750
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PITCHER, EDMUND R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..21
;      OTHER INFORMATION:  /product= "AP1 SEQUENCE"
US-08-507-750-2

  Query Match             100.0%;  Score 20;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.058;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      2 GCTTGATGACTCAGCCGGAA 21


RESULT 3
US-08-764-522A-2
; Sequence 2, Application US/08764522A
; Patent No. 6090544
;  GENERAL INFORMATION:
;    APPLICANT:  HARADA, SHUN-ICHI
;    APPLICANT:  SAMPATH, T. K.
;    APPLICANT:  RODAN, GIDEON A.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR IDENTIFYING
;    TITLE OF INVENTION:  MORPHOGEN ANALOGS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  01748
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,522A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  VITO, CHRISTINE C.
;      REGISTRATION NUMBER:  39,061
;      REFERENCE/DOCKET NUMBER:  CRP-126
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..21
;      OTHER INFORMATION:  /product= "AP1 SEQUENCE A"
US-08-764-522A-2

  Query Match             100.0%;  Score 20;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.058;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          ||||||||||||||||||||
Db      2 GCTTGATGACTCAGCCGGAA 21


RESULT 4
US-08-764-528-2
; Sequence 2, Application US/08764528
; Patent No. 6103491
;  GENERAL INFORMATION:
;    APPLICANT:  SAMPATH, K. T.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR IDENTIFYING
;    TITLE OF INVENTION:  MORPHOGEN ANALOGS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  01748
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,528
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  VITO, CHRISTINE C.
;      REGISTRATION NUMBER:  39,061
```

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;      REFERENCE/DOCKET NUMBER:  CRP-127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..21
;      OTHER INFORMATION:  /product= "AP1 SEQUENCE A"
US-08-764-528-2

  Query Match             100.0%;  Score 20;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.058;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          ||||||||||||||||||||
Db      2 GCTTGATGACTCAGCCGGAA 21


RESULT 5
US-08-872-859-2
; Sequence 2, Application US/08872859
; Patent No. 6110460
;  GENERAL INFORMATION:
;    APPLICANT:  SAMPATH, T. K.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR IDENTIFYING
;    TITLE OF INVENTION:  MORPHOGEN ANALOGS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, TESTA, HURWITZ &
;      ADDRESSEE:  THIBEAULT
;      STREET:  53 STATE STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/872,859
;      FILING DATE:  11-JUN-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/507,750
;      FILING DATE:  26-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PITCHER, EDMUND R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..21
;      OTHER INFORMATION:  /product= "AP1 SEQUENCE"
US-08-872-859-2

  Query Match             100.0%;  Score 20;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.058;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          ||||||||||||||||||||
Db      2 GCTTGATGACTCAGCCGGAA 21


RESULT 6
US-08-283-591-15
; Sequence 15, Application US/08283591
; Patent No. 5629152
;  GENERAL INFORMATION:
;    APPLICANT:  Ravikumar, Vasulinga
;    TITLE OF INVENTION:  NOVEL TRISUBSTITUTED  -LACTAMS AND
;    TITLE OF INVENTION:  OLIGO  -LACTAMAMIDES
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz and
;      ADDRESSEE:  No. 5629152ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,591
;      FILING DATE:  N/A
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
US-08-283-591-15

  Query Match             92.0%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          ||||| ||||||||||||||
Db      2 GCTTGGTGACTCAGCCGGAA 21


RESULT 7
US-08-210-880B-3
; Sequence 3, Application US/08210880B
; Patent No. 5641486
;  GENERAL INFORMATION:
;    APPLICANT:  HINRICHS, STEVEN H.
;    APPLICANT:  ORTEN, DANA J.
;    TITLE OF INVENTION:  METHOD AND COMPOSITION FOR INHIBITING
;    TITLE OF INVENTION:  CREB/ATF1 FAMILY DETERMINED TRANSCRIPTION
```

```
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HENDERSON & STURM
;      STREET:  1125 S. 103RD ST., #330
;      CITY:  OMAHA
;      STATE:  NE
;      COUNTRY:  US
;      ZIP:  68124
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/210,880B
;      FILING DATE:  18-MAR-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JONDLE, ROBERT J.
;      REGISTRATION NUMBER:  33,915
;      REFERENCE/DOCKET NUMBER:  63066
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  402-398-9000
;      TELEFAX:  402-398-9005
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-210-880B-3

  Query Match             92.0%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||| ||||||||||
Db       2 GCTTGATGAGTCAGCCGGAA 21


RESULT 8
US-08-632-275-1/c
; Sequence 1, Application US/08632275
; Patent No. 5840277
;  GENERAL INFORMATION:
;    APPLICANT:  Ghio, Andrew J.
;    APPLICANT:  Kennedy, Thomas P.
;    TITLE OF INVENTION:  Treatment of Chronic Pulmonary
;    TITLE OF INVENTION:  Inflamation
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5840277th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,275
;      FILING DATE:  15-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/413,699
;      FILING DATE:  30-MAR-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lipscomb, Ernest B.
;      REGISTRATION NUMBER:  24,733
;      REFERENCE/DOCKET NUMBER:  8751-5-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  704-331-6000
;      TELEFAX:  704-334-2014
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FRAGMENT TYPE:  linear
US-08-632-275-1

  Query Match             92.0%;  Score 18.4;  DB 2;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           ||||||||| ||||||||||
Db      20 GCTTGATGAGTCAGCCGGAA 1


RESULT 9
US-08-771-411-3
; Sequence 3, Application US/08771411
; Patent No. 5844096
;  GENERAL INFORMATION:
;    APPLICANT:  HINRICHS, STEVEN H.
;    APPLICANT:  ORTEN, DANA J.
;    TITLE OF INVENTION:  METHOD AND COMPOSITION FOR INHIBITING
;    TITLE OF INVENTION:  CREB/ATF1 FAMILY DETERMINED TRANSCRIPTION
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HENDERSON & STURM
;      STREET:  1125 S. 103RD ST., #330
;      CITY:  OMAHA
;      STATE:  NE
;      COUNTRY:  US
;      ZIP:  68124
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,411
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,880
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JONDLE, ROBERT J.
;      REGISTRATION NUMBER:  33,915
;      REFERENCE/DOCKET NUMBER:  63066
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  402-398-9000
;      TELEFAX:  402-398-9005
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-771-411-3

  Query Match             92.0%;  Score 18.4;  DB 2;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy       1 GCTTGATGACTCAGCCGGAA 20
           |||||||||  ||||||||||
Db       2 GCTTGATGAGTCAGCCGGAA 21


RESULT 10
US-09-097-929-1/c
; Sequence 1, Application US/09097929
; Patent No. 6024940
;  GENERAL INFORMATION:
;    APPLICANT:  Ghio, Andrew J.
;    APPLICANT:  Kennedy, Thomas P.
;    TITLE OF INVENTION:  Treatment of Chronic Pulmonary
;    TITLE OF INVENTION:  Inflamation
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6024940th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,929
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,275
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lipscomb, Ernest B.
;      REGISTRATION NUMBER:  24,733
;      REFERENCE/DOCKET NUMBER:  8751-5-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  704-331-6000
;      TELEFAX:  704-334-2014
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FRAGMENT TYPE:  linear
US-09-097-929-1

  Query Match             92.0%;  Score 18.4;  DB 3;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           |||||||||  ||||||||||
Db      20 GCTTGATGAGTCAGCCGGAA 1


RESULT 11
US-09-021-247-8
; Sequence 8, Application US/09021247
; Patent No. 6225444
;  GENERAL INFORMATION:
;    APPLICANT:  Shashoua, Victor E.
;    TITLE OF INVENTION:  NEUROPROTECTIVE PEPTIDES AND USES THEREOF
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/021,247
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  N0260/7023
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
;    HYPOTHETICAL:  NO
US-09-021-247-8

  Query Match             92.0%;  Score 18.4;  DB 4;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           |||||||||  ||||||||||
Db       2 GCTTGATGAGTCAGCCGGAA 21


RESULT 12
US-08-088-661F-8
; Sequence 8, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
;  APPLICANT:  No. 6228982den, Benget
;  APPLICANT:  Wittung, Pernilla
;  APPLICANT:  Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf
;  TITLE OF INVENTION:  Double-Stranded Peptide Nucleic Acids
;  FILE REFERENCE:  ISIS1108
;  CURRENT APPLICATION NUMBER: US/08/088,661F
;  CURRENT FILING DATE:  1993-07-02
;  PRIOR APPLICATION NUMBER:  08/054,363
;  PRIOR FILING DATE:  1993-04-26
;  PRIOR APPLICATION NUMBER:  PCT/EP92/01219
;  PRIOR FILING DATE:  1992-05-19
;  NUMBER OF SEQ ID NOS:  42
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661F-8

  Query Match             92.0%;  Score 18.4;  DB 4;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCTTGATGACTCAGCCGGAA 20
           |||||  ||||||||||||||
Db       2 GCTTGGTGACTCAGCCGGAA 21
```

```
RESULT 13
US-08-088-661F-42
; Sequence 42, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
;  APPLICANT:  No. 6228982den, Benget
;  APPLICANT:  Wittung, Pernilla
;  APPLICANT:  Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf
;  TITLE OF INVENTION:  Double-Stranded Peptide Nucleic Acids
;  FILE REFERENCE:  ISIS1108
;  CURRENT APPLICATION NUMBER: US/08/088,661F
;  CURRENT FILING DATE:  1993-07-02
;  PRIOR APPLICATION NUMBER:  08/054,363
;  PRIOR FILING DATE:  1993-04-26
;  PRIOR APPLICATION NUMBER:  PCT/EP92/01219
;  PRIOR FILING DATE:  1992-05-19
;  NUMBER OF SEQ ID NOS:  42
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661F-42

  Query Match             92.0%;  Score 18.4;  DB 4;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 0.42;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
          ||||| ||||||||||||||
Db      2 GCTTGGTGACTCAGCCGGAA 21


RESULT 14
US-08-203-198-1
; Sequence 1, Application US/08203198
; Patent No. 5512462
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Suzanne
;    TITLE OF INVENTION:  Methods and Reagents for the Polymerase
;    TITLE OF INVENTION:  Chain Reaction Amplification of Long DNA Sequences
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/203,198
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry Ph.D., Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8894
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-203-198-1

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCG 17
          |||| ||||||| ||||
Db      4 GCTTTATGACTCTGCCG 20


RESULT 15
US-07-791-213D-68/c
; Sequence 68, Application US/07791213D
; Patent No. 5409895
;  GENERAL INFORMATION:
;    APPLICANT:  MORISHITA, Hideaki
;    APPLICANT:  KANAMORI, Toshinori
;    APPLICANT:  NOBUHARA, Masahiro
;    TITLE OF INVENTION:  POLYPEPTIDE, DNA FRAGMENT ENCODING THE
;    TITLE OF INVENTION:  SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
;    TITLE OF INVENTION:  INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
;    TITLE OF INVENTION:  TREATING USING THE SAME
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/791,213D
;      FILING DATE:  13-NOV-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-306745
;      FILING DATE:  13-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meuth, Donna M
;      REGISTRATION NUMBER:  36,607
;      REFERENCE/DOCKET NUMBER:  029650-032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  complement (1..26)
US-07-791-213D-68

  Query Match             68.0%;  Score 13.6;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 GCTTGATGACTCAGCCGGAA 20
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Db      26 GCTGGATCCCTCAGCCGAAA 7
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Search completed: December 12, 2002, 01:41:48
Job time : 24.2464 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
(without alignments)
1829.698 Million cell updates/sec

Title: US-09-355-254F-14
Perfect score: 20
Sequence: 1 agcgggggcgagcgggggcg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89793	A89793 Sequence 15
2		20	100.0	20	6	A90880	A90880 Sequence 15
3		20	100.0	20	6	AX023403	AX023403 Sequence
4		20	100.0	20	6	AX455554	AX455554 Sequence
5		20	100.0	30	6	AX472520	AX472520 Sequence
6		20	100.0	30	6	AX476834	AX476834 Sequence
7		20	100.0	30	6	AX476857	AX476857 Sequence
8		16.4	82.0	30	6	AR063474	AR063474 Sequence
9		16.4	82.0	30	6	I28154	I28154 Sequence 11
10		14.2	71.0	47	6	AX128389	AX128389 Sequence
11	c	14.2	71.0	50	6	AR032813	AR032813 Sequence
12	c	14.2	71.0	50	6	AR209477	AR209477 Sequence
13	c	14.2	71.0	50	6	I29553	I29553 Sequence 42
14	c	14.2	71.0	50	6	I91227	I91227 Sequence 42
15	c	14.2	71.0	51	6	AX158283	AX158283 Sequence
16		13.8	69.0	72	9	HSDNASDAE	Z22319 H.sapiens D
17	c	13.8	69.0	100	11	AF235063	AF235063 Mus muscu
18		13.6	68.0	30	6	AX472521	AX472521 Sequence
19		13.6	68.0	30	6	AX476835	AX476835 Sequence
20	c	13.6	68.0	40	6	I86249	I86249 Sequence 3
21		13.6	68.0	44	6	AX157237	AX157237 Sequence
22	c	13.6	68.0	50	10	MMU41966	U41966 Mus musculu
23		13.6	68.0	51	6	A42081	A42081 Sequence 24
24		13.6	68.0	98	6	AR017637	AR017637 Sequence
25		13.6	68.0	98	6	AR094814	AR094814 Sequence
26		13.6	68.0	98	6	AR165473	AR165473 Sequence
27	c	13.6	68.0	99	8	AY033466	AY033466 Zea mays
28		13.6	68.0	100	6	I28243	I28243 Sequence 1
29		13.4	67.0	24	6	AR058202	AR058202 Sequence
30		13.4	67.0	24	6	AR152031	AR152031 Sequence
31		13.4	67.0	24	6	I50793	I50793 Sequence 24
32	c	13.4	67.0	30	6	AX167104	AX167104 Sequence
33		13.4	67.0	33	6	AX202261	AX202261 Sequence
34	c	13.2	66.0	19	6	AX129905	AX129905 Sequence
35	c	13.2	66.0	19	6	AX129926	AX129926 Sequence
36		13.2	66.0	19	6	AX202627	AX202627 Sequence
37		13.2	66.0	21	6	A88115	A88115 Sequence 26
38		13.2	66.0	21	6	A90082	A90082 Sequence 26
39		13.2	66.0	22	6	A33211	A33211 Synthetic H
40	c	13.2	66.0	47	6	AR154447	AR154447 Sequence
41	c	13.2	66.0	50	6	AX159936	AX159936 Sequence
42	c	13.2	66.0	51	6	AX159935	AX159935 Sequence
43		13.2	66.0	54	6	AR032427	AR032427 Sequence
44		13.2	66.0	54	6	AR032648	AR032648 Sequence
45		13.2	66.0	54	6	AR209091	AR209091 Sequence

ALIGNMENTS

RESULT 1
A89793
LOCUS A89793 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 15 from Patent WO9832462.
ACCESSION A89793
VERSION A89793.1 GI:6738307
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 15 30-JUL-1998;

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            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c     14 g      0 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
          ||||||||||||||||||||
Db      1 AGCGGGGGCGAGCGGGGGCG 20


RESULT 2
A90880
LOCUS       A90880                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 15 from Patent EP0855184.
ACCESSION   A90880
VERSION     A90880.1  GI:6739295
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 15 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c     14 g      0 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
          ||||||||||||||||||||
Db      1 AGCGGGGGCGAGCGGGGGCG 20


RESULT 3
AX023403
LOCUS       AX023403                 20 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 18 from Patent WO0014217.
ACCESSION   AX023403
VERSION     AX023403.1  GI:10183803
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipford,G.B., Heeg,K. and Wagner,H.
  TITLE     G-motif oligonucleotides and uses thereof
  JOURNAL   Patent: WO 0014217-A 18 16-MAR-2000;
            LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;
            CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic, no natural origin"
BASE COUNT        2 a      4 c     14 g      0 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
          ||||||||||||||||||||
Db      1 AGCGGGGGCGAGCGGGGGCG 20


RESULT 4
AX455554
LOCUS       AX455554                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 31 from Patent WO0222809.
ACCESSION   AX455554
VERSION     AX455554.1  GI:21714622
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 31 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        2 a      4 c     14 g      0 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
          ||||||||||||||||||||
Db      1 AGCGGGGGCGAGCGGGGGCG 20


RESULT 5
AX472520
LOCUS       AX472520                 30 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 15 from Patent WO02052039.
ACCESSION   AX472520
VERSION     AX472520.1  GI:22207424
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blais,Y., Rousseau,P., Leblanc,B. and Camato,R.N.
  TITLE     Methods for selecting and producing selective pharmaceutical
            compounds and compositions using an established genetically altered
            cell-based library responsive to transcription factors; genetic
            constructs and library therefor
  JOURNAL   Patent: WO 02052039-A 15 04-JUL-2002;
            Geneka Biotechnology Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        5 a      7 c     17 g      1 t
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  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
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              ||||||||||||||||||||
Db      7 AGCGGGGGCGAGCGGGGGCG 26


RESULT 6
AX476834
LOCUS       AX476834                  30 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 11 from Patent WO02052037.
ACCESSION   AX476834
VERSION     AX476834.1  GI:22216110
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Larose,A.M., Rousseau,P., Leblanc,B. and Camato,R.
  TITLE     Method for screening and/or identifying factors that bind to
            nucleic acids
  JOURNAL   Patent: WO 02052037-A 11 04-JUL-2002;
            Geneka Biotechnology Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="NABE-probes"
BASE COUNT        5 a      7 c     17 g      1 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
          ||||||||||||||||||||
Db      7 AGCGGGGGCGAGCGGGGGCG 26


RESULT 7
AX476857
LOCUS       AX476857                  30 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 34 from Patent WO02052037.
ACCESSION   AX476857
VERSION     AX476857.1  GI:22216133
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Larose,A.M., Rousseau,P., Leblanc,B. and Camato,R.
  TITLE     Method for screening and/or identifying factors that bind to
            nucleic acids
  JOURNAL   Patent: WO 02052037-A 34 04-JUL-2002;
            Geneka Biotechnology Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Double stranded NABE"
BASE COUNT        5 a      7 c     17 g      1 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGCGGGGGCGAGCGGGGGCG 20
          ||||||||||||||||||||
Db      7 AGCGGGGGCGAGCGGGGGCG 26


RESULT 8
AR063474
LOCUS       AR063474                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5846706.
ACCESSION   AR063474
VERSION     AR063474.1  GI:5992782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Greenberg,S.J. and Evans,M.Jo.
  TITLE     Rapid and sensitive detection of herpes simplex virus
  JOURNAL   Patent: US 5846706-A 11 08-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        5 a      7 c     18 g      0 t
ORIGIN

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  Best Local Similarity  94.4%;  Pred. No. 4.1e+04;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GCGGGGGCGAGCGGGGGC 19
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Db     12 GCGGGGGCGAGCGGGAGC 29


RESULT 9
I28154
LOCUS       I28154                    30 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 11 from patent US 5569583.
ACCESSION   I28154
VERSION     I28154.1  GI:1818930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Greenberg,S.J. and Evans,M.J.
  TITLE     Rapid and sensitive detection of cytomegalovirus
  JOURNAL   Patent: US 5569583-A 11 29-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        5 a      7 c     18 g      0 t
ORIGIN

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  Best Local Similarity  94.4%;  Pred. No. 4.1e+04;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GCGGGGGCGAGCGGGGGC 19
          ||||||||||||||| ||
Db     12 GCGGGGGCGAGCGGGAGC 29


RESULT 10
AX128389
LOCUS       AX128389                  47 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 50 from Patent WO0130843.
ACCESSION   AX128389
VERSION     AX128389.1  GI:14134897
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Barbas,C.F., Kadan,M. and Beerli,R.
  TITLE     Ligand activated transcriptional regulator proteins
  JOURNAL   Patent: WO 0130843-A 50 03-MAY-2001;
            Novartis AG (CH) ; The Scripps Research Institute (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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BASE COUNT       11 a      11 c      20 g       5 t
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Qy       2 GCGGGGGCGAGCGGGGGCG 20
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Db      20 GCAGGCGCGAGCGTGGGCG 38


RESULT 11
AR032813/c
LOCUS       AR032813                  50 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 425 from patent US 5869241.
ACCESSION   AR032813
VERSION     AR032813.1  GI:5948418
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Method of determining DNA sequence preference of a DNA-binding
            molecule
  JOURNAL   Patent: US 5869241-A 425 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        6 a      23 c      17 g       4 t
ORIGIN

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  Best Local Similarity   84.2%;  Pred. No. 2.3e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GCGGGGGCGAGCGGGGGCG 20
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Db      23 GCGGGGGCGGGGGCGGGCG 5


RESULT 12
AR209477/c
LOCUS       AR209477                  50 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 425 from patent US 6384208.
ACCESSION   AR209477
VERSION     AR209477.1  GI:21510913
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence directed DNA binding molecules compositions and methods
  JOURNAL   Patent: US 6384208-A 425 07-MAY-2002;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        6 a      23 c      17 g       4 t
ORIGIN

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  Best Local Similarity   84.2%;  Pred. No. 2.3e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GCGGGGGCGAGCGGGGGCG 20
           ||||||||| | | |||||
Db      23 GCGGGGGCGGGGGCGGGCG 5


RESULT 13
I29553/c
LOCUS       I29553                    50 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 425 from patent US 5578444.
ACCESSION   I29553
VERSION     I29553.1  GI:1820344
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence-directed DNA-binding molecules compositions and methods
  JOURNAL   Patent: US 5578444-A 425 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        6 a      23 c      17 g       4 t
ORIGIN

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  Best Local Similarity   84.2%;  Pred. No. 2.3e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GCGGGGGCGAGCGGGGGCG 20
           ||||||||| | | |||||
Db      23 GCGGGGGCGGGGGCGGGCG 5


RESULT 14
I91227/c
LOCUS       I91227                    50 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 425 from patent US 5726014.
ACCESSION   I91227
VERSION     I91227.1  GI:3935697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
  TITLE     Screening assay for the detection of DNA-binding molecules
  JOURNAL   Patent: US 5726014-A 425 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        6 a      23 c      17 g       4 t
ORIGIN

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  Best Local Similarity   84.2%;  Pred. No. 2.3e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GCGGGGGCGAGCGGGGGCG 20
           ||||||||| | | |||||
Db      23 GCGGGGGCGGGGGCGGGCG 5


RESULT 15
AX158283/c
LOCUS       AX158283                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1611 from Patent WO0140521.
ACCESSION   AX158283
VERSION     AX158283.1  GI:14539614
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
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  JOURNAL   Patent: WO 0140521-A 1611 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (1612 is other entry)
                     Accession number cg32120097"
BASE COUNT        6 a     22 c     15 g      8 t
ORIGIN

  Query Match             71.0%;  Score 14.2;  DB 6;  Length 51;
  Best Local Similarity   84.2%;  Pred. No. 2.2e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 AGCGGGGGCGAGCGGGGGC 19
           ||| ||||| |||||| ||
Db      43 AGCCGGGGCCAGCGGGAGC 25


Search completed: December 12, 2002, 02:55:54
Job time : 323.116 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:07:11 ; Search time 815.797 Seconds
(without alignments)
397.047 Million cell updates/sec

Title: US-09-355-254F-8
Perfect score: 20
Sequence: 1 gattgcctgacgtcagagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14.2	71.0	78	17	AZ871578	AZ871578 2M0184G04
c	2	13.4	67.0	50	17	AZ492887	AZ492887 1M0327F13
c	3	13.2	66.0	49	17	BH861707	BH861707 SALK_0878
c	4	13.2	66.0	50	9	AU107195	AU107195 AU107195
c	5	13.2	66.0	67	9	AA721395	AA721395 nz73g08.s
c	6	13.2	66.0	71	9	AA702828	AA702828 zi77b06.s
c	7	13.2	66.0	91	17	AZ512653	AZ512653 1M0358G22
	8	13.2	66.0	93	9	AA560086	AA560086 v129c05.r
c	9	13.2	66.0	99	12	BF458655	BF458655 UI-M-BZ1-
c	10	12.8	64.0	34	17	AQ073796	AQ073796 EP(3)3179
c	11	12.8	64.0	40	9	AA848120	AA848120 oe05a03.s
c	12	12.8	64.0	50	9	AU105994	AU105994 AU105994
	13	12.8	64.0	69	17	BH256492	BH256492 KG03686-5
	14	12.8	64.0	86	9	AI204909	AI204909 an05g11.x
c	15	12.8	64.0	88	9	AU260302	AU260302 AU260302
c	16	12.8	64.0	99	14	F26219	F26219 HSPD13614 H
	17	12.6	63.0	73	10	BE095402	BE095402 SWOvMfCAR
	18	12.6	63.0	73	17	BH862484	BH862484 SALK_0900
	19	12.6	63.0	81	9	AA580289	AA580289 nn12d02.s
c	20	12.6	63.0	84	10	AV952690	AV952690 AV952690
	21	12.6	63.0	84	17	AZ312968	AZ312968 1M0029D10
c	22	12.6	63.0	91	17	AZ494456	AZ494456 1M0329D13
	23	12.6	63.0	95	17	AZ810623	AZ810623 2M0076G18
c	24	12.6	63.0	98	17	BH853467	BH853467 SALK_0770
c	25	12.4	62.0	93	14	W31755	W31755 zb93d09.r1
	26	12.4	62.0	94	17	AZ763191	AZ763191 1M0558K01
	27	12.2	61.0	43	17	BH796799	BH796799 1008096G1
c	28	12.2	61.0	50	9	AU107190	AU107190 AU107190
c	29	12.2	61.0	50	9	AU107194	AU107194 AU107194
c	30	12.2	61.0	50	9	AU107198	AU107198 AU107198
c	31	12.2	61.0	54	17	AZ776635	AZ776635 2M0010M22
c	32	12.2	61.0	55	17	AZ920728	AZ920728 1006022C0
c	33	12.2	61.0	64	9	AI253600	AI253600 aq31f10.x
	34	12.2	61.0	64	13	BI698792	BI698792 Ts699 The
c	35	12.2	61.0	74	9	AA218675	AA218675 zq14f10.s
	36	12.2	61.0	79	9	AA600457	AA600457 vm78f05.r
	37	12.2	61.0	80	9	AA985780	AA985780 ua66f08.r
c	38	12.2	61.0	82	14	W05256	W05256 za84b06.r1
	39	12.2	61.0	83	9	AA075933	AA075933 zm76e12.r
c	40	12.2	61.0	85	9	AA716566	AA716566 zg70e03.s
c	41	12.2	61.0	88	17	AZ430802	AZ430802 1M0215M19
c	42	12.2	61.0	90	12	BG400826	BG400826 602464048
	43	12.2	61.0	97	14	H28506	H28506 yl59e08.r1
	44	12.2	61.0	100	13	BI002964	BI002964 MR3-HN006
c	45	12.2	61.0	100	17	AZ780127	AZ780127 2M0017J11

ALIGNMENTS

RESULT 1
AZ871578/c
LOCUS AZ871578 78 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0184G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184G04 R, DNA sequence.
ACCESSION AZ871578
VERSION AZ871578.1 GI:13077918
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 78)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0184 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 78.

FEATURES Location/Qualifiers
source 1. .78
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0184G04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 23 a 19 c 15 g 21 t
ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 78;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GATTGCCTGACGTCAGAGA 19
           ||| ||| || ||||||||
Db      52 GATAGCCAGAAGTCAGAGA 34
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RESULT 2
AZ492887/c
LOCUS AZ492887 50 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0327F13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0327F13 F, DNA sequence.
ACCESSION AZ492887
VERSION AZ492887.1 GI:10666029
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0327 row: F column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 50.

FEATURES Location/Qualifiers
source 1. .50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0327F13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 17 c 13 g 17 t
ORIGIN

Query Match 67.0%; Score 13.4; DB 17; Length 50;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       4 TGCCTGACGTCAGAG 18
           ||||||||| |||||
Db      16 TGCCTGACGGCAGAG 2
```

RESULT 3
BH861707/c
LOCUS BH861707 49 bp DNA linear GSS 05-AUG-2002
DEFINITION SALK_087868 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_087868, DNA sequence.
ACCESSION BH861707
VERSION BH861707.1 GI:22097033
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 49)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g49230.

```
          Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_087868"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       16 a     14 c      7 g     12 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 17;  Length 49;
  Best Local Similarity   83.3%;  Pred. No. 2.8e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 ATTGCCTGACGTCAGAGA 19
           ||| | |||||| |||||
Db      36 ATTCCTTGACGTGAGAGA 19


RESULT 4
AU107195/c
LOCUS       AU107195                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107195 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP21410, mRNA sequence.
ACCESSION   AU107195
VERSION     AU107195.1  GI:13556716
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HEP21410"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT       12 a     14 c     14 g     10 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 9;  Length 50;
  Best Local Similarity   83.3%;  Pred. No. 2.8e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           ||| |||||||||  |||
Db      41 TTGGCTGACGTCAACGAG 24


RESULT 5
AA721395/c
LOCUS       AA721395                 67 bp    mRNA    linear   EST 23-JAN-1998
DEFINITION  nz73g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301150 3',
            mRNA sequence.
ACCESSION   AA721395
VERSION     AA721395.1  GI:2737530
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 67)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 835   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 57.
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1301150"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       14 a     24 c     15 g     14 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 9;  Length 67;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAG 18
           |||||| ||||  |||||
Db      30 GATTGCTTGACCCCAGAG 13


RESULT 6
AA702828/c
LOCUS       AA702828                 71 bp    mRNA    linear   EST 19-DEC-1997
DEFINITION  zi77b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:436787 3' similar to contains element CER repetitive
            element ;, mRNA sequence.
ACCESSION   AA702828
VERSION     AA702828.1  GI:2705941
```

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 68.
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="Homo sapiens"
                     /db_xref="GDB:1336556"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:436787"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       14 a     17 c     20 g     20 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 9;  Length 71;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAG 18
          |||  ||||| |||||||
Db     60 GATCACCTGAGGTCAGAG 43


RESULT 7
AZ512653/c
LOCUS       AZ512653                 91 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0358G22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0358G22 F, DNA sequence.
ACCESSION   AZ512653
VERSION     AZ512653.1  GI:10693969
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0358  row: G  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 91.
FEATURES             Location/Qualifiers
     source          1. .91
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0358G22"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       19 a     19 c     39 g     14 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 17;  Length 91;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 TTGCCTGACGTCAGAGAG 20
          |||||||  | |||||  ||
Db     75 TTGCCTGGCCTCAGATAG 58


RESULT 8
AA560086
LOCUS       AA560086                 93 bp    mRNA    linear   EST 18-AUG-1997
DEFINITION  vl29c05.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
            IMAGE:973640 5', mRNA sequence.
ACCESSION   AA560086
VERSION     AA560086.1  GI:2331551
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
```

```
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:554368
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 85.
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:973640"
                     /clone_lib="Stratagene mouse Tcell 937311"
                     /tissue_type="Tcell"
                     /dev_stage="M30 CD4+ cells"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT       22 a     17 c     28 g     26 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 9;  Length 93;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 ATTGCCTGACGTCAGAGA 19
           || || ||| ||||||||
Db      62 ATGGCTTGATGTCAGAGA 79


RESULT 9
BF458655/c
LOCUS       BF458655                 99 bp    mRNA    linear   EST 01-DEC-2000
DEFINITION  UI-M-BZ1-blt-g-01-0-UI.s1 NIH_BMAP_MHI2_S1 Mus musculus cDNA clone
            UI-M-BZ1-blt-g-01-0-UI 3', mRNA sequence.
ACCESSION   BF458655
VERSION     BF458655.1  GI:11524824
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            hippocampus tissue cDNA Library Preparation: M.B. Soares Lab Clone
            distribution: Researchers may obtain BMAP cDNA clones from RESEARCH
            GENETICS. It should be noted that Bento Soares is generating a
            small number of additional specialized non-redundant arrays of BMAP
            cDNAs whose availability will be considered under appropriate and
            limited collaborative arrangements The following repetitive
            elements were found in this cDNA sequence: 1-21,
            >AT_rich#Low_complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BZ1-blt-g-01-0-UI"
                     /clone_lib="NIH_BMAP_MHI2_S1"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_MHI2_S1 library is a subtracted library derived
                     from  NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived
                     from mouse hippocampus tissue. For a detailed description
                     of the library from which this clone was  derived, please
                     visit our web site at brainest.eng.uiowa.edu.
                     TAG_LIB=NIH_BMAP_MHI2_S1
                     TAG_TISSUE=hippocampus
                     TAG_SEQ=TAGCC"
BASE COUNT       18 a     26 c     32 g     23 t
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 12;  Length 99;
  Best Local Similarity   83.3%;  Pred. No. 3.7e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           |||||||  || ||||||
Db      57 TTGCCTGGGGTGAGAGAG 40


RESULT 10
AQ073796/c
LOCUS       AQ073796                 34 bp    DNA     linear   GSS 23-AUG-2000
DEFINITION  EP(3)3179 Drosophila melanogaster EP line Drosophila melanogaster
            genomic Sequence recovered from Both 5' and 3' ends of P element,
            DNA sequence.
ACCESSION   AQ073796
VERSION     AQ073796.1  GI:3403838
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Liao,G.-C., Rehm,E.J. and Rubin,G.M.
  TITLE     Insertion site preferences of the P transposable element in
            Drosophila melanogaster
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
  MEDLINE   20202638
COMMENT     Contact: Gerald Rubin
            Berkeley Drosophila Genome Project
            University of California, Berkeley
            LSA Building, Berkeley, CA 94720-3200, USA
            Fax: 5106439947
            Email: gerry@fruitfly.berkeley.edu
            Sequence recovery method was inverse PCR.

            Sequence orientation is forward strand relative to 5' end of P
            element

            The P element insertion position is base 15 in the 34 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.
            Class: transposon-tagged.
```

```
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster EP line"
                     /note="Inverse PCR was performed on Drosophila
                     melanogaster strains each of which contains a single EP
                     transposable element insertion. (The generation of these
                     insertion strains is described in Rorth P, Szabo K, Bailey
                     A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
                     V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
                     genetics in Drosophila. Development 6:1049-1057.) The
                     resultant fragment for each strain was directly sequenced
                     to determine the genomic sequence at the site of
                     insertion. Details of the protocols used can be found at
                     http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
BASE COUNT        4 a     11 c     10 g      9 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 17;  Length 34;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 GCCTGACGTCAGAGAG 20
           || |||||| ||||||
Db      32 GCGTGACGTGAGAGAG 17


RESULT 11
AA848120/c
LOCUS       AA848120                 40 bp    mRNA    linear   EST 07-APR-1998
DEFINITION  oe05a03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1384972
            similar to gb:M35663 INTERFERON-INDUCED, DOUBLE-STRANDED
            RNA-ACTIVATED PROTEIN KINASE (HUMAN);, mRNA sequence.
ACCESSION   AA848120
VERSION     AA848120.1  GI:2934638
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1464   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1384972"
                     /clone_lib="NCI_CGAP_Ov2"
                     /sex="female"
                     /tissue_type="ovary"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from invasive ovarian
                     tumor, cDNA made by oligo-dT priming.  Non-directionally
                     cloned. Size-selected on agarose gel, average insert  size
                     600 bp. Reference:  Krizman et al. (1996) Cancer Research
                     56:5380-5383."
BASE COUNT        8 a     14 c      9 g      9 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 40;
  Best Local Similarity   87.5%;  Pred. No. 3.9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAG 16
           |||||| ||| |||||
Db      40 GATTGCTTGAGGTCAG 25


RESULT 12
AU105994/c
LOCUS       AU105994                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU105994 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAIA2602, mRNA sequence.
ACCESSION   AU105994
VERSION     AU105994.1  GI:13555515
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAIA2602"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT       11 a     19 c      9 g     11 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAG 16
           ||| |||||| |||||
Db      29 GATCGCCTGAGGTCAG 14


RESULT 13
BH256492
LOCUS       BH256492                 69 bp    DNA     linear   GSS 29-NOV-2001
DEFINITION  KG03686-5prime Drosophila melanogaster P{SUPor-P} P element
            insertion lines Drosophila melanogaster genomic Sequence recovered
            from 5' end of P element, DNA sequence.
ACCESSION   BH256492
VERSION     BH256492.1  GI:17151385
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
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            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Levis,R., Hoskins,R., Liao,G., Mozden,N., Tsang,G., He,Y., Karpen
            ,G., Bellen,H., Rubin,G. and Spradling,A.
  TITLE     The Berkeley Drosophila Genome Project Gene Disruption Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Gerald Rubin
            Berkeley Drosophila Genome Project
            University of California, Berkeley
            LSA Building, Berkeley, CA 94720-3200, USA
            Fax: 5106439947
            Email: gerry@fruitfly.berkeley.edu
            Sequence recovery method was inverse PCR.
            Sequence orientation is forward strand relative to 5' end of P
            element
            The P element insertion position is base 62 in the 69 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster P{SUPor-P} P element
                     insertion lines"
                     /note="Inverse PCR was performed on Drosophila
                     melanogaster strains each of which contains one or more
                     P{SUPor-P} P-element transposon insertion. The resultant
                     fragment for each strain was directly sequenced to
                     determine the genomic sequence at the site of insertion.
                     Details of the protocols used can be found at
                     http://www.fruitfly.org/about/methods/inverse.pcr.html."
BASE COUNT       15 a     15 c     18 g     21 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 17;  Length 69;
  Best Local Similarity   87.5%;  Pred. No. 4.9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 ATTGCCTGACGTCAGA 17
           ||||| ||| ||||||
Db       2 ATTGCGTGAAGTCAGA 17


RESULT 14
AI204909
LOCUS       AI204909                 86 bp    mRNA    linear   EST 15-OCT-1998
DEFINITION  an05g11.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone
            IMAGE:1684772 3' similar to gb:M55053 CYTOCHROME P450 IA2 (HUMAN);,
            mRNA sequence.
ACCESSION   AI204909
VERSION     AI204909.1  GI:3757971
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .86
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1684772"
                     /clone_lib="Stratagene schizo brain S11"
                     /sex="male"
                     /tissue_type="schizophrenic brain S-11 frontal lobe"
                     /dev_stage="34 years old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI;  Library
                     constructed from S-11 frontal lobe, male, 34 years old,
                     50% caucasian, 50% Aleutian.  Schizophrenic suicide.
                     Random primed into EcoRI site of ZAP II Vector.  Mass
                     excised. Custom library. Avg insert length 1.4kb.
                     Material obtained by Johnston N., Torrey, E.F., Yolken R.,
                     and the Stanley Neuropathology Consortium - Analysis of
                     RNAs from the Brains of Individuals with Psychiatric
                     Diseases (Unpublished) Stanley Neurovirology Laboratory,
                     Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT       26 a     19 c     24 g     17 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 86;
  Best Local Similarity   87.5%;  Pred. No. 5.4e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 GCCTGACGTCAGAGAG 20
           ||||| || |||||||
Db      43 GCCTGGCGACAGAGAG 58


RESULT 15
AU260302/c
LOCUS       AU260302                 88 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU260302 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0016644 3', mRNA sequence.
ACCESSION   AU260302
VERSION     AU260302.1  GI:20327661
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .88
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="BED0016644"
                     /clone_lib="3'-directed mouse cDNA library"
                     /tissue_type="brain"
                     /note="Vector: pGEM-T-easy"
BASE COUNT       27 a     26 c     19 g     16 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 88;
  Best Local Similarity   87.5%;  Pred. No. 5.4e+04;
```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       5 GCCTGACGTCAGAGAG 20
           ||||||  ||||||||
Db      19 GCCTGAACTCAGAGAG 4
```

Search completed: December 12, 2002, 06:03:49
Job time : 834.154 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:12:31 ; Search time 33.8406 Seconds
(without alignments)
233.720 Million cell updates/sec

Title: US-09-355-254F-8
Perfect score: 20
Sequence: 1 gattgcctgacgtcagagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 212722

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	27	10	US-09-878-918-2	Sequence 2, Appli
	2	19	95.0	23	10	US-09-816-763-148	Sequence 148, App
	3	12.8	64.0	50	10	US-09-875-945-4	Sequence 4, Appli
	4	12.8	64.0	97	10	US-09-864-761-19704	Sequence 19704, A
	5	12.6	63.0	57	10	US-09-969-192-60	Sequence 60, Appl
c	6	12.6	63.0	57	10	US-09-969-192-61	Sequence 61, Appl
	7	12.6	63.0	63	10	US-09-969-192-58	Sequence 58, Appl
c	8	12.6	63.0	86	10	US-09-983-965-5019	Sequence 5019, Ap
	9	12.2	61.0	18	10	US-09-420-433-62	Sequence 62, Appl
c	10	12.2	61.0	24	10	US-09-784-911-30	Sequence 30, Appl
	11	12.2	61.0	99	10	US-09-769-066-11	Sequence 11, Appl
	12	12	60.0	63	10	US-09-998-598-2339	Sequence 2339, Ap
	13	12	60.0	86	9	US-10-040-497-79	Sequence 79, Appl
	14	12	60.0	92	10	US-09-864-761-28968	Sequence 28968, A
	15	11.8	59.0	18	8	US-08-983-605-140	Sequence 140, App
	16	11.6	58.0	18	10	US-09-303-510-50	Sequence 50, Appl
	17	11.6	58.0	18	10	US-09-303-040-50	Sequence 50, Appl
c	18	11.6	58.0	20	9	US-10-060-301-123	Sequence 123, App
c	19	11.6	58.0	41	10	US-09-238-351-29	Sequence 29, Appl
c	20	11.6	58.0	41	10	US-09-238-351-40	Sequence 40, Appl
c	21	11.6	58.0	59	9	US-09-933-797-527	Sequence 527, App
	22	11.6	58.0	64	10	US-09-983-965-5569	Sequence 5569, Ap
	23	11.6	58.0	76	10	US-09-864-761-32057	Sequence 32057, A
	24	11.6	58.0	90	10	US-09-864-761-19844	Sequence 19844, A
	25	11.6	58.0	91	10	US-09-864-761-32056	Sequence 32056, A
	26	11.6	58.0	93	10	US-09-864-761-28341	Sequence 28341, A
c	27	11.6	58.0	98	10	US-09-864-761-26316	Sequence 26316, A
	28	11.4	57.0	23	10	US-09-893-238-22	Sequence 22, Appl
	29	11.4	57.0	47	9	US-09-853-526-242	Sequence 242, App
	30	11.4	57.0	47	10	US-09-901-484A-242	Sequence 242, App
	31	11.4	57.0	99	10	US-09-864-761-20908	Sequence 20908, A
	32	11.2	56.0	25	9	US-09-764-868-1251	Sequence 1251, Ap
	33	11.2	56.0	26	9	US-10-113-877-145	Sequence 145, App
c	34	11.2	56.0	31	10	US-09-801-274-276	Sequence 276, App
c	35	11.2	56.0	44	10	US-09-875-519A-14	Sequence 14, Appl
c	36	11.2	56.0	47	9	US-09-853-526-319	Sequence 319, App
c	37	11.2	56.0	47	10	US-09-901-484A-319	Sequence 319, App
	38	11.2	56.0	59	10	US-09-875-945-12	Sequence 12, Appl
	39	11.2	56.0	84	10	US-09-764-860-1052	Sequence 1052, Ap
	40	11.2	56.0	84	10	US-09-764-860-1053	Sequence 1053, Ap
	41	11.2	56.0	84	10	US-09-764-877-3676	Sequence 3676, Ap
	42	11.2	56.0	88	10	US-09-764-869-1992	Sequence 1992, Ap
	43	11.2	56.0	88	10	US-09-764-869-1993	Sequence 1993, Ap
c	44	11.2	56.0	89	10	US-09-764-887-567	Sequence 567, App
	45	11.2	56.0	91	10	US-09-764-847-1964	Sequence 1964, Ap

ALIGNMENTS

RESULT 1
US-09-878-918-2
; Sequence 2, Application US/09878918
; Patent No. US20020107193A1
; GENERAL INFORMATION:
; APPLICANT: Glazner Dr., Gordon W
; TITLE OF INVENTION: Therapeutic uses for IP3 receptor-mediated calcium
; TITLE OF INVENTION: channel modulators
; FILE REFERENCE: 84894-602
; CURRENT APPLICATION NUMBER: US/09/878,918
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/246763
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CREB binding
; OTHER INFORMATION: site
US-09-878-918-2

Query Match 100.0%; Score 20; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTGCCTGACGTCAGAGAG 20
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Db 4 GATTGCCTGACGTCAGAGAG 23

RESULT 2
US-09-816-763-148
; Sequence 148, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE

```
;  TITLE OF INVENTION:  DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
;  TITLE OF INVENTION:  FACTORS
;  FILE REFERENCE: VANM212.001AUS
;  CURRENT APPLICATION NUMBER: US/09/816,763
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: EP 00870057.7
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CREB consensus sequence
US-09-816-763-148

  Query Match             95.0%;  Score 19;  DB 10;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ATTGCCTGACGTCAGAGAG 20
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Db      1 ATTGCCTGACGTCAGAGAG 19


RESULT 3
US-09-875-945-4
; Sequence 4, Application US/09875945
; Patent No. US20020098169A1
; GENERAL INFORMATION:
;  APPLICANT: METCON MEDICIN AB
;  APPLICANT:  SMITH, Ulf
;  TITLE OF INVENTION: No. US20020098169A1el sequences and their use
;  FILE REFERENCE: 45513MH
;  CURRENT APPLICATION NUMBER: US/09/875,945
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: SE 0002189-9
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: US 60/210,207
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-875-945-4

  Query Match             64.0%;  Score 12.8;  DB 10;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 9.4e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAG 16
          |||||| ||| |||||
Db      6 GATTGCTTGAGGTCAG 21


RESULT 4
US-09-864-761-19704
; Sequence 19704, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19704
;   LENGTH: 97
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC009490.4
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
;   OTHER INFORMATION: NT HIT: X56160.1, EVALUE 3.20e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AV648669.1, EVALUE 1.90e-02
US-09-864-761-19704

  Query Match             64.0%;  Score 12.8;  DB 10;  Length 97;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      5 GCCTGACGTCAGAGAG 20
          ||| ||| ||||||||
Db     74 GCCAGACATCAGAGAG 89


RESULT 5
US-09-969-192-60
; Sequence 60, Application US/09969192
; Patent No. US20020151027A1
;   GENERAL INFORMATION:
;        APPLICANT: WICKHAM, THOMAS J.
;                   ROELVINK, PETRUS W.
```

```
;                KOVESDI, IMRE
;       TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;                           CONSTRAINED PEPTIDE MOTIFS
;       NUMBER OF SEQUENCES: 80
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;            STREET: Two Prudential Plaza - 49th Floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60601
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/969,192
;            FILING DATE: 01-Oct-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 9-455061
;            FILING DATE: 06-DEC-1999
;            APPLICATION NUMBER: US 9-130225
;            FILING DATE: 06-AUG-1998
;            APPLICATION NUMBER: US 8-701124
;            FILING DATE: 21-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hefner, M. Daniel
;            REGISTRATION NUMBER: 41,826
;            REFERENCE/DOCKET NUMBER: 213564
;   INFORMATION FOR SEQ ID NO: 60:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 57 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-969-192-60

  Query Match             63.0%;  Score 12.6;  DB 10;  Length 57;
  Best Local Similarity   78.9%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 ATTGCCTGACGTCAGAGAG 20
           | | | ||||||| |||||
Db       8 AATTCTTGACGTCGGAGAG 26


RESULT 6
US-09-969-192-61/c
; Sequence 61, Application US/09969192
; Patent No. US20020151027A1
;   GENERAL INFORMATION:
;       APPLICANT: WICKHAM, THOMAS J.
;                  ROELVINK, PETRUS W.
;                  KOVESDI, IMRE
;       TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;                           CONSTRAINED PEPTIDE MOTIFS
;       NUMBER OF SEQUENCES: 80
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;            STREET: Two Prudential Plaza - 49th Floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60601
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/969,192
;            FILING DATE: 01-Oct-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 9-455061
;            FILING DATE: 06-DEC-1999
;            APPLICATION NUMBER: US 9-130225
;            FILING DATE: 06-AUG-1998
;            APPLICATION NUMBER: US 8-701124
;            FILING DATE: 21-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hefner, M. Daniel
;            REGISTRATION NUMBER: 41,826
;            REFERENCE/DOCKET NUMBER: 213564
;   INFORMATION FOR SEQ ID NO: 61:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 57 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-969-192-61

  Query Match             63.0%;  Score 12.6;  DB 10;  Length 57;
  Best Local Similarity   78.9%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 ATTGCCTGACGTCAGAGAG 20
           | | | ||||||| |||||
Db      54 AATTCTTGACGTCGGAGAG 36


RESULT 7
US-09-969-192-58
; Sequence 58, Application US/09969192
; Patent No. US20020151027A1
;   GENERAL INFORMATION:
;       APPLICANT: WICKHAM, THOMAS J.
;                  ROELVINK, PETRUS W.
;                  KOVESDI, IMRE
;       TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;                           CONSTRAINED PEPTIDE MOTIFS
;       NUMBER OF SEQUENCES: 80
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;            STREET: Two Prudential Plaza - 49th Floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60601
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/969,192
;            FILING DATE: 01-Oct-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 9-455061
;            FILING DATE: 06-DEC-1999
;            APPLICATION NUMBER: US 9-130225
;            FILING DATE: 06-AUG-1998
;            APPLICATION NUMBER: US 8-701124
;            FILING DATE: 21-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hefner, M. Daniel
;            REGISTRATION NUMBER: 41,826
;            REFERENCE/DOCKET NUMBER: 213564
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 63 base pairs
;            TYPE: nucleic acid
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;             STRANDEDNESS: double
;             TOPOLOGY: linear
;          MOLECULE TYPE: DNA (genomic)
;          SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-969-192-58

  Query Match             63.0%;  Score 12.6;  DB 10;  Length 63;
  Best Local Similarity   78.9%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ATTGCCTGACGTCAGAGAG 20
          | | | ||||||| |||||
Db      9 AATTCTTGACGTCGGAGAG 27


RESULT 8
US-09-983-965-5019/c
; Sequence 5019, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 37-21(10297)C
;  CURRENT APPLICATION NUMBER: US/09/983,965
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: US 09/465,231
;  PRIOR FILING DATE: 1999-12-15
;  PRIOR APPLICATION NUMBER: US 60/113,678
;  PRIOR FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5019
;   LENGTH: 86
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 29-LIB34-022-Q1-E1-H1
US-09-983-965-5019

  Query Match             63.0%;  Score 12.6;  DB 10;  Length 86;
  Best Local Similarity   78.9%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGA 19
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Db     61 GATGGCCTGGGGTCAAAGA 43


RESULT 9
US-09-420-433-62
; Sequence 62, Application US/09420433
; Patent No. US20020098480A1
;  GENERAL INFORMATION:
;    APPLICANT:  Sidransky, David
;    TITLE OF INVENTION:  NUCLEIC ACID MUTATION DETECTION IN
;    TITLE OF INVENTION:  HISTOLOGIC TISSUE
;    NUMBER OF SEQUENCES:  82
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/420,433
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/181,664
;      FILING DATE:  JANUARY 14, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wetherell, Jr., Ph.D., John R.
;      REGISTRATION NUMBER:  31,678
;      REFERENCE/DOCKET NUMBER:  PD-3055
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..18
US-09-420-433-62

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 1.7e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 TGCCTGACGTCAGAGAG 20
          |||||| |||  |||||
Db      1 TGCCTGTCGTGGGAGAG 17


RESULT 10
US-09-784-911-30/c
; Sequence 30, Application US/09784911
; Patent No. US20020072115A1
; GENERAL INFORMATION:
;  APPLICANT: Harrison, Leonard C.
;  APPLICANT:  Jiang, Fang-Xu
;  APPLICANT:  Stanley, Edouard Guy
;  APPLICANT:  Gonez, Leonel Jorge
;  TITLE OF INVENTION: Pancreatic islet cell growth factors
;  FILE REFERENCE: Davies Collison Cave
;  CURRENT APPLICATION NUMBER: US/09/784,911
;  CURRENT FILING DATE:  2001-09-17
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 2.1
; SEQ ID NO 30
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: primer
US-09-784-911-30

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 24;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 TGCCTGACGTCAGAGAG 20
          ||| |||| ||| ||||
Db     17 TGCGTGACATCAAAGAG 1


RESULT 11
US-09-769-066-11
; Sequence 11, Application US/09769066
; Patent No. US20020107360A1
;  GENERAL INFORMATION:
;       APPLICANT: Fuerst, Thomas R.
;                  McAtee, C. Patrick
;                  Yarbough, Patrice O.
;                  Zhang, Yifan
```

```
;       TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
;       NUMBER OF SEQUENCES: 31
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dehlinger & Associates
;            STREET: 350 Cambridge Ave., Suite 250
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94306
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/769,066
;            FILING DATE: 24-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/542,634
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Fabian, Gary R.
;            REGISTRATION NUMBER: 33,875
;            REFERENCE/DOCKET NUMBER: 4600-0293.30
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 324-0880
;            TELEFAX: (415) 324-0960
;   INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 99 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: Hepatitis E Virus (Burma strain)
;                          406.4-2 region
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ORIGINAL SOURCE:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-769-066-11

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 99;
  Best Local Similarity   82.4%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGA 19
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Db      58 TTGCCTCACGTCGTAGA 74


RESULT 12
US-09-998-598-2339
; Sequence 2339, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
;  APPLICANT: Stolk, John A.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Chenault, Ruth A.
;  APPLICANT:  Meagher, Madelein Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.561
;  CURRENT APPLICATION NUMBER: US/09/998,598
;  CURRENT FILING DATE:  2001-11-16
;  NUMBER OF SEQ ID NOS: 2606
;  SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 2339
;   LENGTH: 63
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-998-598-2339

  Query Match             60.0%;  Score 12;  DB 10;  Length 63;
  Best Local Similarity   75.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGAG 20
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Db      14 GAACTCCTGACGTCAAAGTG 33


RESULT 13
US-10-040-497-79
; Sequence 79, Application US/10040497
; Patent No. US20020172962A1
;   GENERAL INFORMATION:
;       APPLICANT: GOLD, LARRY
;                  TUERK, CRAIG
;       TITLE OF INVENTION: METHODS OF PRODUCING NUCLEIC ACID LIGANDS
;       NUMBER OF SEQUENCES: 83
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Swanson & Bratschun, L.L.C.
;            STREET: 8400 E. Prentice Avenue, Suite 200
;            CITY: Englewood
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
;            COMPUTER: IBM compatible
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: WordPerfect 8.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/040,497
;            FILING DATE: 07-Jan-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/748,697
;            FILING DATE: 13-NOVEMBER-1996
;            APPLICATION NUMBER: 08/442,062
;            FILING DATE: 16-MAY-1995
;            APPLICATION NUMBER: 07/964,624
;            FILING DATE: 21-OCTOBER-1992
;            APPLICATION NUMBER: 07/714,131
;            FILING DATE: 10-JUNE-1991
;            APPLICATION NUMBER: 07/536,428
;            FILING DATE: 11-JUNE-1990
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Barry J. Swanson
;            REGISTRATION NUMBER: 33,215
;            REFERENCE/DOCKET NUMBER: NEX05/DC-CON
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (303) 793-3333
;            TELEFAX: (303) 793-3433
;   INFORMATION FOR SEQ ID NO: 79:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 86 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-040-497-79

  Query Match             60.0%;  Score 12;  DB 9;  Length 86;
  Best Local Similarity   65.0%;  Pred. No. 2.5e+03;
  Matches   13;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGAG 20
           ||: |||:  || | |||||
Db      10 GAUGGCCUUCCGACCGAGAG 29


RESULT 14
US-09-864-761-28968
; Sequence 28968, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28968
;   LENGTH: 92
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL136112.9
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.83
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: NT HIT: gi|1420890, EVALUE 4.00e-15
;   OTHER INFORMATION: EST_HUMAN HIT: BF209778.1, EVALUE 4.00e-34
;   OTHER INFORMATION: SWISSPROT HIT: P36198, EVALUE 4.90e-01
US-09-864-761-28968

  Query Match             60.0%;  Score 12;  DB 10;  Length 92;
  Best Local Similarity   75.0%;  Pred. No. 2.5e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGAG 20
           || |||  |||| ||||| |
Db      61 GACTGCTAGACGCCAGAGGG 80
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RESULT 15
US-08-983-605-140
; Sequence 140, Application US/08983605A
; Patent No. US20020066118A1
; GENERAL INFORMATION:
;  APPLICANT: Roder, Marion
;  TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
;  TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of
;  TITLE OF INVENTION: Said Markers
;  FILE REFERENCE: 2936.10400
;  CURRENT APPLICATION NUMBER: US/08/983,605A
;  CURRENT FILING DATE: 1998-05-01
;  EARLIER APPLICATION NUMBER: DE 195 25 284.5
;  EARLIER FILING DATE: 1995-06-28
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-08-983-605-140

  Query Match             59.0%;  Score 11.8;  DB 8;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 2.7e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       6 CCTGACGTCAGAGAG 20
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Db       4 CCCCACGTCAGAGAG 18


Search completed: December 12, 2002, 06:12:14
Job time : 42.0549 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:05:40 ; Search time 22.2464 Seconds
(without alignments)
275.709 Million cell updates/sec

Title: US-09-355-254F-8
Perfect score: 20
Sequence: 1 gattgcctgacgtcagagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	2	US-09-133-774-10	Sequence 10, Appl
	2	20	100.0	20	3	US-09-303-862-10	Sequence 10, Appl
	3	20	100.0	27	1	US-08-210-880B-2	Sequence 2, Appli
	4	20	100.0	27	2	US-08-771-411-2	Sequence 2, Appli
	5	16.4	82.0	32	4	US-09-215-098-1	Sequence 1, Appli
	6	16.4	82.0	50	1	US-08-171-389-451	Sequence 451, App
	7	16.4	82.0	50	1	US-08-123-936-451	Sequence 451, App
	8	16.4	82.0	50	2	US-08-475-228A-451	Sequence 451, App
	9	16.4	82.0	50	3	US-08-482-080A-451	Sequence 451, App
	10	16.4	82.0	50	4	US-09-354-947-451	Sequence 451, App
	11	16.4	82.0	50	5	PCT-US93-12388-451	Sequence 451, App
c	12	14.2	71.0	41	3	US-08-813-507-78	Sequence 78, Appl
c	13	14.2	71.0	41	4	US-09-464-453-78	Sequence 78, Appl
	14	13.8	69.0	71	4	US-08-870-930-25	Sequence 25, Appl
	15	13.8	69.0	71	4	US-09-254-968-28	Sequence 28, Appl
c	16	12.8	64.0	61	3	US-09-023-228B-89	Sequence 89, Appl
c	17	12.8	64.0	61	4	US-09-163-025B-89	Sequence 89, Appl
	18	12.6	63.0	57	2	US-08-701-124-60	Sequence 60, Appl
c	19	12.6	63.0	57	2	US-08-701-124-61	Sequence 61, Appl
	20	12.6	63.0	57	3	US-09-130-225-60	Sequence 60, Appl
c	21	12.6	63.0	57	3	US-09-130-225-61	Sequence 61, Appl
	22	12.6	63.0	57	4	US-09-455-061-60	Sequence 60, Appl
c	23	12.6	63.0	57	4	US-09-455-061-61	Sequence 61, Appl
	24	12.6	63.0	63	2	US-08-701-124-58	Sequence 58, Appl
	25	12.6	63.0	63	3	US-09-130-225-58	Sequence 58, Appl
	26	12.6	63.0	63	4	US-09-455-061-58	Sequence 58, Appl
c	27	12.6	63.0	98	1	US-08-441-430-5	Sequence 5, Appli
c	28	12.4	62.0	27	2	US-08-244-434-13	Sequence 13, Appl
	29	12.4	62.0	35	2	US-08-244-434-12	Sequence 12, Appl
	30	12.4	62.0	35	2	US-08-244-434-16	Sequence 16, Appl
c	31	12.4	62.0	40	2	US-09-130-114-18	Sequence 18, Appl
	32	12.4	62.0	44	2	US-09-130-114-17	Sequence 17, Appl
	33	12.2	61.0	18	1	US-08-152-313-89	Sequence 89, Appl
	34	12.2	61.0	18	1	US-08-579-223-89	Sequence 89, Appl
	35	12.2	61.0	18	3	US-08-181-664-62	Sequence 62, Appl
	36	12.2	61.0	18	5	PCT-US94-12947A-89	Sequence 89, Appl
c	37	12.2	61.0	20	4	US-09-122-171D-15	Sequence 15, Appl
	38	12.2	61.0	21	4	US-09-324-867-43	Sequence 43, Appl
c	39	12.2	61.0	22	3	US-08-840-316-95	Sequence 95, Appl
c	40	12.2	61.0	22	4	US-08-809-523-95	Sequence 95, Appl
c	41	12.2	61.0	22	4	US-08-471-971-95	Sequence 95, Appl
c	42	12.2	61.0	22	4	US-09-402-776-95	Sequence 95, Appl
c	43	12.2	61.0	22	5	PCT-US93-08849A-95	Sequence 95, Appl
c	44	12.2	61.0	22	5	PCT-US93-08849-95	Sequence 95, Appl
	45	12.2	61.0	25	1	US-07-991-466-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-133-774-10
; Sequence 10, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Hear
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-133-774-10

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTGCCTGACGTCAGAGAG 20
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Db 1 GATTGCCTGACGTCAGAGAG 20

RESULT 2
US-09-303-862-10
; Sequence 10, Application US/09303862
; Patent No. 6034230
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Hear
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774

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;  EARLIER FILING DATE: 1998-08-12
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia trachomatis
;   FEATURE:
;   OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
;   OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
;   OTHER INFORMATION: Chlamydia trachomatis.
US-09-303-862-10

  Query Match             100.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      1 GATTGCCTGACGTCAGAGAG 20


RESULT 3
US-08-210-880B-2
; Sequence 2, Application US/08210880B
; Patent No. 5641486
;  GENERAL INFORMATION:
;    APPLICANT:  HINRICHS, STEVEN H.
;    APPLICANT:  ORTEN, DANA J.
;    TITLE OF INVENTION:  METHOD AND COMPOSITION FOR INHIBITING
;    TITLE OF INVENTION:  CREB/ATF1 FAMILY DETERMINED TRANSCRIPTION
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HENDERSON & STURM
;      STREET:  1125 S. 103RD ST., #330
;      CITY:  OMAHA
;      STATE:  NE
;      COUNTRY:  US
;      ZIP:  68124
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/210,880B
;      FILING DATE:  18-MAR-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JONDLE, ROBERT J.
;      REGISTRATION NUMBER:  33,915
;      REFERENCE/DOCKET NUMBER:  63066
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  402-398-9000
;      TELEFAX:  402-398-9005
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-210-880B-2

  Query Match             100.0%;  Score 20;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 4
US-08-771-411-2
; Sequence 2, Application US/08771411
; Patent No. 5844096
;  GENERAL INFORMATION:
;    APPLICANT:  HINRICHS, STEVEN H.
;    APPLICANT:  ORTEN, DANA J.
;    TITLE OF INVENTION:  METHOD AND COMPOSITION FOR INHIBITING
;    TITLE OF INVENTION:  CREB/ATF1 FAMILY DETERMINED TRANSCRIPTION
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HENDERSON & STURM
;      STREET:  1125 S. 103RD ST., #330
;      CITY:  OMAHA
;      STATE:  NE
;      COUNTRY:  US
;      ZIP:  68124
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,411
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,880
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JONDLE, ROBERT J.
;      REGISTRATION NUMBER:  33,915
;      REFERENCE/DOCKET NUMBER:  63066
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  402-398-9000
;      TELEFAX:  402-398-9005
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-771-411-2

  Query Match             100.0%;  Score 20;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 5
US-09-215-098-1
; Sequence 1, Application US/09215098
; Patent No. 6194632
; GENERAL INFORMATION:
;  APPLICANT:  Leiden, Jeffery M
;  TITLE OF INVENTION:  DILATED CARDIOMYOPATHY IN TRANSGENIC MICE EXPRESSING A
;  TITLE OF INVENTION:  DOMINANT-NEGATIVE CREB TRANSCRIPTION FACTOR IN THE
;  TITLE OF INVENTION:  HEART
;  FILE REFERENCE:  9189-4
;  CURRENT APPLICATION NUMBER: US/09/215,098
;  CURRENT FILING DATE:  1998-12-18
;  PRIOR APPLICATION NUMBER:  60/068,011
;  PRIOR FILING DATE:  1997-12-18
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 32
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
;   OTHER INFORMATION: containing the CREB site from the somatostatin
;   OTHER INFORMATION: promoter
US-09-215-098-1

  Query Match             82.0%;  Score 16.4;  DB 4;  Length 32;
  Best Local Similarity   94.4%;  Pred. No. 4.9;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
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Db      11 TTGGCTGACGTCAGAGAG 28


RESULT 6
US-08-171-389-451
; Sequence 451, Application US/08171389
; Patent No. 5578444
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/171,389
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0175/G19P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  451:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human somatostatin I gene
US-08-171-389-451

  Query Match             82.0%;  Score 16.4;  DB 1;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           | ||||||||||||||||
Db       1 TAGCCTGACGTCAGAGAG 18


RESULT 7
US-08-123-936-451
; Sequence 451, Application US/08123936
; Patent No. 5726014
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    TITLE OF INVENTION:  Screening Assay for the Detection of
;    TITLE OF INVENTION:  DNA-Binding Molecules
;    NUMBER OF SEQUENCES:  640
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/123,936
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0075.32/G19P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  451:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human somatostatin I gene
US-08-123-936-451

  Query Match             82.0%;  Score 16.4;  DB 1;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           | ||||||||||||||||
Db       1 TAGCCTGACGTCAGAGAG 18
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```
RESULT 8
US-08-475-228A-451
; Sequence 451, Application US/08475228A
; Patent No. 5869241
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,228A
;      FILING DATE:  06-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stratford, Carol A.
;      REGISTRATION NUMBER:  34,444
;      REFERENCE/DOCKET NUMBER:  4600-0175.21/G19P3D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  451:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human somatostatin I gene
US-08-475-228A-451

  Query Match             82.0%;  Score 16.4;  DB 2;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           | ||||||||||||||||
Db       1 TAGCCTGACGTCAGAGAG 18


RESULT 9
US-08-482-080A-451
; Sequence 451, Application US/08482080A
; Patent No. 6010849
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,080A
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/171,389
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brady, John F.
;      REGISTRATION NUMBER:  39,118
;      REFERENCE/DOCKET NUMBER:  4600-0175.20/G19P3D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  451:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human somatostatin I gene
US-08-482-080A-451

  Query Match             82.0%;  Score 16.4;  DB 3;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           | ||||||||||||||||
Db       1 TAGCCTGACGTCAGAGAG 18


RESULT 10
US-09-354-947-451
; Sequence 451, Application US/09354947
; Patent No. 6384208
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
```

```
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/354,947
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/482,080
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/171,389
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brady, John F.
;      REGISTRATION NUMBER:  39,118
;      REFERENCE/DOCKET NUMBER:  4600-0175.20/G19P3D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  451:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human somatostatin I gene
US-09-354-947-451

  Query Match             82.0%;  Score 16.4;  DB 4;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           | ||||||||||||||||
Db       1 TAGCCTGACGTCAGAGAG 18


RESULT 11
PCT-US93-12388-451
; Sequence 451, Application PC/TUS9312388
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12388
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0175.41/G19PCT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  451:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human somatostatin I gene
PCT-US93-12388-451

  Query Match             82.0%;  Score 16.4;  DB 5;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 TTGCCTGACGTCAGAGAG 20
           | ||||||||||||||||
Db       1 TAGCCTGACGTCAGAGAG 18


RESULT 12
US-08-813-507-78/c
; Sequence 78, Application US/08813507
; Patent No. 6114116
;  GENERAL INFORMATION:
;    APPLICANT:  Lemieux, Bertrand
;    APPLICANT:  Landry, Benoit S.
;    APPLICANT:  Sapolsky, Ronald J.
;    TITLE OF INVENTION:  Brassica Polymorphisms
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
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;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/813,507
;       FILING DATE:  07-MAR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/032,069
;       FILING DATE:  02-DEC-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Liebeschuetz, Joe
;       REGISTRATION NUMBER:  37,505
;       REFERENCE/DOCKET NUMBER:  018547-030100US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415 576-0200
;       TELEFAX:  415 576-0200
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  78:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  41 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-813-507-78

  Query Match             71.0%;  Score 14.2;  DB 3;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGA 19
           | || | ||||||||||||
Db      19 GCTTTCATGACGTCAGAGA 1


RESULT 13
US-09-464-453-78/c
; Sequence 78, Application US/09464453
; Patent No. 6358686
;   GENERAL INFORMATION:
;        APPLICANT: Lemieux, Bertrand
;                   Landry, Benoit S.
;                   Sapolsky, Ronald J.
;        TITLE OF INVENTION: Brassica Polymorphisms
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/464,453
;             FILING DATE: 14-Dec-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/813,507
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-030100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415 576-0200
;             TELEFAX: 415 576-0200
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 78:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 41 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-464-453-78

  Query Match             71.0%;  Score 14.2;  DB 4;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGA 19
           | || | ||||||||||||
Db      19 GCTTTCATGACGTCAGAGA 1


RESULT 14
US-08-870-930-25
; Sequence 25, Application US/08870930
; Patent No. 6168778
;  GENERAL INFORMATION:
;    APPLICANT:  NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGEESE, MICHA
;    TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
;    TITLE OF INVENTION:  NUCLEIC ACID LIGAND COMPLEXES
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson and Bratschun, L.L.C.
;      STREET:  8400 East Prentice Avenue, Suite #200
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.4 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 8.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/870,930
;      FILING DATE:  6 JUNE 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX61
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
;    FEATURE:
;      OTHER INFORMATION:  All pyrimidines are 2'-fluoro
US-08-870-930-25

  Query Match             69.0%;  Score 13.8;  DB 4;  Length 71;
  Best Local Similarity   64.7%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGA 17
           ||:: ||:| ||:||||
Db      43 GAUUUCCUGCCGUCAGA 59


RESULT 15
US-09-254-968-28
; Sequence 28, Application US/09254968
; Patent No. 6426335
;   GENERAL INFORMATION:
;        APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGEESE,
```

; MICHAEL WILLIS
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEIC
; ACID LIGAND COMPLEXES
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM compatible
; (C) OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,968
; FILING DATE: 13-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18944
; FILING DATE: 17 OCTOBER 1997
; APPLICATION NUMBER: 08/739,109
; FILING DATE: 25 OCTOBER 1996
; APPLICATION NUMBER: 08/870,930
; FILING DATE: 6 JUNE 1997
; APPLICATION NUMBER: 08/897,351
; FILING DATE: 21 JULY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX61C/PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
; modified
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-254-968-28

Query Match 69.0%; Score 13.8; DB 4; Length 71;
Best Local Similarity 64.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 GATTGCCTGACGTCAGA 17
           ||:: ||:| ||:||||
Db      43 GAUUUCCUGCCGUCAGA 59
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Search completed: December 12, 2002, 01:41:42
Job time : 24.2464 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
(without alignments)
1829.698 Million cell updates/sec

Title: US-09-355-254F-13
Perfect score: 20
Sequence: 1 tgcagattgcgcaatctgca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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29: em_vi:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89792	A89792 Sequence 14
2	c	20	100.0	20	6	A89792	A89792 Sequence 14
3		20	100.0	20	6	A90879	A90879 Sequence 14
4	c	20	100.0	20	6	A90879	A90879 Sequence 14
5		20	100.0	20	6	AR148641	AR148641 Sequence
6	c	20	100.0	20	6	AR148641	AR148641 Sequence
7		20	100.0	20	6	AX455640	AX455640 Sequence
8	c	20	100.0	20	6	AX455640	AX455640 Sequence
9		15.4	77.0	24	6	AX384713	AX384713 Sequence
10	c	15.4	77.0	24	6	AX384713	AX384713 Sequence
11		13.6	68.0	90	6	AR024336	AR024336 Sequence
12	c	13.6	68.0	90	6	AR024336	AR024336 Sequence
13		13.6	68.0	90	6	AR045189	AR045189 Sequence
14	c	13.6	68.0	90	6	AR045189	AR045189 Sequence
15		13.6	68.0	90	6	BD011413	BD011413 Chimeric
16	c	13.6	68.0	90	6	BD011413	BD011413 Chimeric
17		13.6	68.0	90	6	E43883	E43883 Chimeric an
18	c	13.6	68.0	90	6	E43883	E43883 Chimeric an
19		13.4	67.0	28	6	AR202106	AR202106 Sequence
20	c	13.4	67.0	28	6	AR202106	AR202106 Sequence
21		13.2	66.0	21	6	AR041200	AR041200 Sequence
22	c	13.2	66.0	21	6	AR041200	AR041200 Sequence
23		13.2	66.0	21	6	AR116609	AR116609 Sequence
24	c	13.2	66.0	21	6	AR116609	AR116609 Sequence
25		13.2	66.0	21	6	AR159952	AR159952 Sequence
26	c	13.2	66.0	21	6	AR159952	AR159952 Sequence
27		13.2	66.0	21	6	AX268106	AX268106 Sequence
28	c	13.2	66.0	21	6	AX268106	AX268106 Sequence
29		13.2	66.0	33	6	I65281	I65281 Sequence 3
30	c	13.2	66.0	33	6	I65281	I65281 Sequence 3
31		13.2	66.0	54	6	AX244174	AX244174 Sequence
32	c	13.2	66.0	54	6	AX244174	AX244174 Sequence
33		13.2	66.0	59	6	AX015212	AX015212 Sequence
34	c	13.2	66.0	59	6	AX015212	AX015212 Sequence
35		13.2	66.0	59	6	E64355	E64355 Single-stra
36	c	13.2	66.0	59	6	E64355	E64355 Single-stra
37		13.2	66.0	90	6	AX287868	AX287868 Sequence
38	c	13.2	66.0	90	6	AX287868	AX287868 Sequence
39		12.8	64.0	56	6	A62184	A62184 Sequence 78
40	c	12.8	64.0	56	6	A62184	A62184 Sequence 78
41		12.8	64.0	56	6	AR077589	AR077589 Sequence
42	c	12.8	64.0	56	6	AR077589	AR077589 Sequence
43		12.8	64.0	56	6	AX022408	AX022408 Sequence
44	c	12.8	64.0	56	6	AX022408	AX022408 Sequence
45		12.8	64.0	56	6	AX047755	AX047755 Sequence

ALIGNMENTS

RESULT 1
A89792
LOCUS A89792 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 14 from Patent WO9832462.
ACCESSION A89792
VERSION A89792.1 GI:6738306
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 14 30-JUL-1998;

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          LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db      1 TGCAGATTGCGCAATCTGCA 20


RESULT 2
A89792/c
LOCUS       A89792                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 14 from Patent WO9832462.
ACCESSION   A89792
VERSION     A89792.1  GI:6738306
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipford,G.B. and Heeg,K.
  TITLE     PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
            OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
  JOURNAL   Patent: WO 9832462-A 14 30-JUL-1998;
            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db     20 TGCAGATTGCGCAATCTGCA 1


RESULT 3
A90879
LOCUS       A90879                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 14 from Patent EP0855184.
ACCESSION   A90879
VERSION     A90879.1  GI:6739288
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 14 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db      1 TGCAGATTGCGCAATCTGCA 20


RESULT 4
A90879/c
LOCUS       A90879                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 14 from Patent EP0855184.
ACCESSION   A90879
VERSION     A90879.1  GI:6739288
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 14 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db     20 TGCAGATTGCGCAATCTGCA 1


RESULT 5
AR148641
LOCUS       AR148641                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6225444.
ACCESSION   AR148641
VERSION     AR148641.1  GI:15112731
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shashoua,V.E.
  TITLE     Neuroprotective peptides and uses thereof
  JOURNAL   Patent: US 6225444-A 7 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db      1 TGCAGATTGCGCAATCTGCA 20


RESULT 6
AR148641/c
LOCUS       AR148641                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6225444.
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ACCESSION   AR148641
VERSION     AR148641.1  GI:15112731
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shashoua,V.E.
  TITLE     Neuroprotective peptides and uses thereof
  JOURNAL   Patent: US 6225444-A 7 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db     20 TGCAGATTGCGCAATCTGCA 1


RESULT 7
AX455640
LOCUS       AX455640                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 117 from Patent WO0222809.
ACCESSION   AX455640
VERSION     AX455640.1  GI:21714708
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 117 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db      1 TGCAGATTGCGCAATCTGCA 20


RESULT 8
AX455640/c
LOCUS       AX455640                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 117 from Patent WO0222809.
ACCESSION   AX455640
VERSION     AX455640.1  GI:21714708
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 117 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        5 a      5 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCTGCA 20
          ||||||||||||||||||||
Db     20 TGCAGATTGCGCAATCTGCA 1


RESULT 9
AX384713
LOCUS       AX384713                 24 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 4 from Patent WO0181375.
ACCESSION   AX384713
VERSION     AX384713.1  GI:19577904
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schepartz Shrader,A., Chin,J.W., Zutshi,R., Rutledge,S.E., Kehlbeck
            Martin,J.D. and Zondlo,N.J.
  TITLE     Dna & protein binding miniature proteins
  JOURNAL   Patent: WO 0181375-A 4 01-NOV-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Recognition site of CEBP24 protein"
BASE COUNT        5 a      5 c      8 g      6 t
ORIGIN

  Query Match             77.0%;  Score 15.4;  DB 6;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 5.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TGCAGATTGCGCAATCT 17
          || |||||||||||||
Db      3 TGGAGATTGCGCAATCT 19


RESULT 10
AX384713/c
LOCUS       AX384713                 24 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 4 from Patent WO0181375.
ACCESSION   AX384713
VERSION     AX384713.1  GI:19577904
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schepartz Shrader,A., Chin,J.W., Zutshi,R., Rutledge,S.E., Kehlbeck
            Martin,J.D. and Zondlo,N.J.
  TITLE     Dna & protein binding miniature proteins
  JOURNAL   Patent: WO 0181375-A 4 01-NOV-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Recognition site of CEBP24 protein"
BASE COUNT        5 a      5 c      8 g      6 t
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ORIGIN

  Query Match            77.0%;  Score 15.4;  DB 6;  Length 24;
  Best Local Similarity  94.1%;  Pred. No. 5.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 AGATTGCGCAATCTGCA 20
           ||||||||||||||| ||
Db      19 AGATTGCGCAATCTCCA 3


RESULT 11
AR024336
LOCUS       AR024336                  90 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 104 from patent US 5795965.
ACCESSION   AR024336
VERSION     AR024336.1  GI:3977630
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and
            Saldanha,J.William.
  TITLE     Reshaped human to human interleukin-6 receptor
  JOURNAL   Patent: US 5795965-A 104 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="unknown"
BASE COUNT       18 a     22 c     29 g     21 t
ORIGIN

  Query Match            68.0%;  Score 13.6;  DB 6;  Length 90;
  Best Local Similarity  80.0%;  Pred. No. 4.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TGCAGATTGCGCAATCTGCA 20
           ||||| ||| ||| |||| |
Db      11 TGCAGCTTGTGCAGTCTGGA 30


RESULT 12
AR024336/c
LOCUS       AR024336                  90 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 104 from patent US 5795965.
ACCESSION   AR024336
VERSION     AR024336.1  GI:3977630
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and
            Saldanha,J.William.
  TITLE     Reshaped human to human interleukin-6 receptor
  JOURNAL   Patent: US 5795965-A 104 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="unknown"
BASE COUNT       18 a     22 c     29 g     21 t
ORIGIN

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  Best Local Similarity  80.0%;  Pred. No. 4.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TGCAGATTGCGCAATCTGCA 20
           | |||| ||| ||| |||||
Db      30 TCCAGACTGCACAAGCTGCA 11


RESULT 13
AR045189
LOCUS       AR045189                  90 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 104 from patent US 5817790.
ACCESSION   AR045189
VERSION     AR045189.1  GI:5966654
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and
            Saldanha,J.William.
  TITLE     Reshaped human antibody to human interleukin-6 receptor
  JOURNAL   Patent: US 5817790-A 104 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .90
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BASE COUNT       18 a     22 c     29 g     21 t
ORIGIN

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  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TGCAGATTGCGCAATCTGCA 20
           ||||| ||| ||| |||| |
Db      11 TGCAGCTTGTGCAGTCTGGA 30


RESULT 14
AR045189/c
LOCUS       AR045189                  90 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 104 from patent US 5817790.
ACCESSION   AR045189
VERSION     AR045189.1  GI:5966654
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and
            Saldanha,J.William.
  TITLE     Reshaped human antibody to human interleukin-6 receptor
  JOURNAL   Patent: US 5817790-A 104 06-OCT-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT       18 a     22 c     29 g     21 t
ORIGIN

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  Best Local Similarity  80.0%;  Pred. No. 4.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TGCAGATTGCGCAATCTGCA 20
           | |||| ||| ||| |||||
Db      30 TCCAGACTGCACAAGCTGCA 11


RESULT 15
BD011413
LOCUS       BD011413                  90 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Chimeric antibody against human interleukin-6 receptor.
ACCESSION   BD011413
VERSION     BD011413.1  GI:18639786
KEYWORDS    JP 2001083151-A/87.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Tsuchiya,M., Sato,K., Bendigu,M.M., Jones,S.T. and Saldanha,H.W.
  TITLE     Chimeric antibody against human interleukin-6 receptor
  JOURNAL   Patent: JP 2001083151-A 87 30-MAR-2001;
            CHUGAI PHARMACEUTICAL CO LTD
```

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COMMENT     OS-  Artificial Sequence
            PN   JP 2001083151-A/87
            PD   30-MAR-2001
            PF   28-JUL-2000 JP 2000229748
            PR
            PI   MASAYUKI TSUCHIYA,KO SATO,MARY MARGARET BENDIGU, PI   STEVEN
            TAREN JONES,
            PI   HOSE WILLIAM SALDANHA
            PC   G01N33/53,A61K38/00,A61K39/395,A61K39/395,A61P35/00, PC
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            PC   C07K19/00,C12N15/09,(C12N15/09,C12R1:91),A61K37/02,C12N15/00,
            PC   (C12N15/00,C12R1:91)
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                    /db_xref="taxon:32630"
BASE COUNT       18 a     22 c     29 g     21 t
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  Best Local Similarity   80.0%;  Pred. No. 4.4e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TGCAGATTGCGCAATCTGCA 20
           ||||| ||| ||| |||| |
Db      11 TGCAGCTTGTGCAGTCTGGA 30


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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Title: US-09-355-254F-9
Perfect score: 18
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Scoring table: IDENTITY_NUC
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		18	100.0	18	6	A89788	A89788 Sequence 10
2		18	100.0	18	6	A90875	A90875 Sequence 10
3		18	100.0	18	6	AX455583	AX455583 Sequence
4	c	13.8	76.7	38	6	I56082	I56082 Sequence 10
5	c	13.8	76.7	89	6	AX438437	AX438437 Sequence
6	c	13.2	73.3	82	9	HUMMACAJ	L37722 Homo sapien
7	c	13.2	73.3	88	10	MMALDRED04	U89144 Mus musculu
8		13	72.2	89	10	MMTCRAC2	X02846 M.musculus
9		12.8	71.1	29	6	AX099976	AX099976 Sequence
10		12.8	71.1	50	6	A16634	A16634 Nucleotide
11		12.8	71.1	50	6	A16645	A16645 Nucleotide
12	c	12.4	68.9	26	6	AX419077	AX419077 Sequence
13	c	12.4	68.9	51	6	AX204048	AX204048 Sequence
14		12.4	68.9	67	9	HSMYO7A55	U61467 Human myosi
15		12.4	68.9	70	6	AR092212	AR092212 Sequence
16		12.4	68.9	85	6	AX360360	AX360360 Sequence
17		12.2	67.8	30	6	AX469615	AX469615 Sequence
18		12.2	67.8	50	6	AX165806	AX165806 Sequence
19	c	12.2	67.8	51	6	AX165000	AX165000 Sequence
20		12.2	67.8	89	6	AR045019	AR045019 Sequence
21		12.2	67.8	89	6	I18551	I18551 Sequence 20
22		12.2	67.8	89	6	I34095	I34095 Sequence 20
23	c	12.2	67.8	94	1	ECWITA	X75467 E. coli wit
24	c	12.2	67.8	98	11	MMSTS6	Z36555 M.musculus
25	c	12.2	67.8	98	14	AF264011	AF264011 Hepatitis
26		12.2	67.8	100	5	XLRPS4	X64205 X.laevis mR
27		12.2	67.8	100	5	XLRPS11	X64208 X.laevis mR
28		12	66.7	56	6	A43627	A43627 Sequence 17
29	c	12	66.7	92	6	AX193249	AX193249 Sequence
30		12	66.7	94	6	AX396657	AX396657 Sequence
31	c	11.8	65.6	26	6	I23392	I23392 Sequence 10
32	c	11.8	65.6	28	6	E38332	E38332 Process for
33		11.8	65.6	47	6	AX194676	AX194676 Sequence
34	c	11.8	65.6	52	6	E21658	E21658 Spermatogen
35	c	11.8	65.6	74	12	AF405700	AF405700 Synthetic
36	c	11.8	65.6	75	10	MUSIGHCA1	M31028 Mus musculu
37	c	11.8	65.6	77	6	AR081580	AR081580 Sequence
38		11.8	65.6	98	6	AX107888	AX107888 Sequence
39		11.6	64.4	25	6	AR089894	AR089894 Sequence
40		11.6	64.4	25	6	AR196929	AR196929 Sequence
41	c	11.6	64.4	25	6	AX116304	AX116304 Sequence
42	c	11.6	64.4	51	6	AX116305	AX116305 Sequence
43		11.6	64.4	51	6	AX158271	AX158271 Sequence
44		11.6	64.4	51	6	AX158272	AX158272 Sequence
45	c	11.6	64.4	51	6	AX204448	AX204448 Sequence

ALIGNMENTS

RESULT 1
A89788
LOCUS A89788 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 10 from Patent WO9832462.
ACCESSION A89788
VERSION A89788.1 GI:6738302
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 10 30-JUL-1998;

```
          LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      6 g      5 t
ORIGIN

  Query Match           100.0%;  Score 18;  DB 6;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          ||||||||||||||||||
Db      1 GGAATGACGTTCCCTGTG 18


RESULT 2
A90875
LOCUS       A90875                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 10 from Patent EP0855184.
ACCESSION   A90875
VERSION     A90875.1  GI:6739272
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 10 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      6 g      5 t
ORIGIN

  Query Match           100.0%;  Score 18;  DB 6;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          ||||||||||||||||||
Db      1 GGAATGACGTTCCCTGTG 18


RESULT 3
AX455583
LOCUS       AX455583                 18 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 60 from Patent WO0222809.
ACCESSION   AX455583
VERSION     AX455583.1  GI:21714651
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 60 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        3 a      4 c      6 g      5 t
ORIGIN

  Query Match           100.0%;  Score 18;  DB 6;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 23;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          ||||||||||||||||||
Db      1 GGAATGACGTTCCCTGTG 18


RESULT 4
I56082/c
LOCUS       I56082                   38 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 10 from patent US 5648465.
ACCESSION   I56082
VERSION     I56082.1  GI:2476876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Margolis,R.U., Rauch,U. and Margolis,R.K.
  TITLE     Cloning and expression of neurocan, a chondroitin sulfate
            proteoglycan
  JOURNAL   Patent: US 5648465-A 10 15-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="unknown"
BASE COUNT        7 a      9 c      5 g     10 t      7 others
ORIGIN

  Query Match           76.7%;  Score 13.8;  DB 6;  Length 38;
  Best Local Similarity  70.6%;  Pred. No. 6.9e+03;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGT 17
          ||||:||:|| || ||:
Db     38 GGAAYGAYGTNCCNTGY 22


RESULT 5
AX438437/c
LOCUS       AX438437                 89 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 6852 from Patent WO0229113.
ACCESSION   AX438437
VERSION     AX438437.1  GI:21663245
KEYWORDS    .
SOURCE      Bacillus clausii.
  ORGANISM  Bacillus clausii
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1
  AUTHORS   Berka,R. and Clausen,I.G.
  TITLE     Methods for monitoring multiple gene expression
  JOURNAL   Patent: WO 0229113-A 6852 11-APR-2002;
            Novozymes Biotech, Inc. (US) ; Novozymes A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .89
                     /organism="Bacillus clausii"
                     /db_xref="taxon:79880"
BASE COUNT       21 a     16 c     29 g     23 t
ORIGIN

  Query Match           76.7%;  Score 13.8;  DB 6;  Length 89;
  Best Local Similarity  88.2%;  Pred. No. 6.5e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 GAATGACGTTCCCTGTG 18
          ||| ||| |||||||||
Db     88 GAAAGACATTCCCTGTG 72


RESULT 6
HUMMACAJ/c
LOCUS       HUMMACAJ                 82 bp    mRNA    linear   PRI 11-JAN-1995
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DEFINITION  Homo sapiens (clone 10) macronuclear mRNA.
ACCESSION   L37722
VERSION     L37722.1  GI:576851
KEYWORDS    macronuclear.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 82)
  AUTHORS   Carney,J.P., McKnight,C.E., VanEpps,S. and Kelley,M.R.
  TITLE     Random amplification of cDNA ends (RRACE) allows for cloning of
            multiple novel human cDNA fragments containing CAG repeats
  JOURNAL   Gene (1994) In press
COMMENT     clones were isolated using a CAG oligo.  The oligo was made up of
            CAG x 8,
            so by definition the first 24 bases are CAG x 8 (not included in
            the
            database entries).  The actual number of CAG's is undetermined.
FEATURES             Location/Qualifiers
     source          1. .82
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="#10"
                     /cell_line="Jurkat"
     mRNA            1. .82
BASE COUNT       20 a     29 c     21 g     10 t      2 others
ORIGIN

  Query Match             73.3%;  Score 13.2;  DB 9;  Length 82;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGAATGACGTTCCCTGTG 18
           ||  ||| ||||||||||
Db      64 GGCCTGAGGTTCCCTGTG 47


RESULT 7
MMALDRED04/c
LOCUS       MMALDRED04               88 bp    DNA     linear   ROD 13-APR-1998
DEFINITION  Mus musculus aldose reductase gene, exon 4.
ACCESSION   U89144
VERSION     U89144.1  GI:3046239
KEYWORDS    .
SEGMENT     4 of 10
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   McGowan,M.H., Iwata,T. and Carper,D.A.
  TITLE     Characterization of the mouse aldose reductase gene and promoter in
            a lens epithelial cell line
  JOURNAL   Mol. Vis. 4, 2 (1998)
  MEDLINE   98153248
   PUBMED   9485485
  REMARK    http://www.emory.edu/molvis/v4/p2
REFERENCE   2  (bases 1 to 88)
  AUTHORS   McGowan,M.H., Iwata,T. and Carper,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-1997) LMOD, National Eye Institute, 9000
            Rockville Pike, Bldg6/Rm232, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .88
                     /organism="Mus musculus"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /chromosome="6"
     exon            5. .82
                     /number=4
BASE COUNT       21 a     23 c     24 g     20 t
ORIGIN

  Query Match             73.3%;  Score 13.2;  DB 10;  Length 88;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GGAATGACGTTCCCTGTG 18
           || ||  |||||||||| |
Db      51 GGTATCACGTTCCCTGAG 34


RESULT 8
MMTCRAC2
LOCUS       MMTCRAC2                 89 bp    DNA     linear   ROD 02-FEB-1995
DEFINITION  M.musculus gene for Tcell receptor alpha-chain constant region exon
            2.
ACCESSION   X02846
VERSION     X02846.1  GI:54472
KEYWORDS    constant region; T-cell receptor.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 89)
  AUTHORS   Hayday,A.C., Diamond,D.J., Tanigawa,G., Heilig,J.S., Folsom,V.,
            Saito,H. and Tonegawa,S.
  TITLE     Unusual organization and diversity of T-cell receptor alpha-chain
            genes
  JOURNAL   Nature 316 (6031), 828-832 (1985)
  MEDLINE   85296331
   PUBMED   2993907
COMMENT     The coding sequence is identical to that of alpha-chain mRNA
            isolated from cytotoxic T-cells (clone pHDS58, see X01134). The
            first base of the first codon of PHDS58 constant region is
            identical to pos. 91 in X02843.
FEATURES             Location/Qualifiers
     source          1. .89
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /cell_type="lymphocyte T"
     intron          <1. .21
                     /note="intron"
     C_region        22. .66
                     /product="constant region of Tcell alpha chain"
                     /note="exon 2"
     intron          67. .>89
                     /note="intron"
BASE COUNT       23 a     20 c     21 g     25 t
ORIGIN

  Query Match             72.2%;  Score 13;  DB 10;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 GACGTTCCCTGTG 18
           !!!!!!!!!!!!!
Db      21 GACGTTCCCTGTG 33


RESULT 9
AX099976
LOCUS       AX099976                 29 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 5 from Patent WO0120007.
ACCESSION   AX099976
VERSION     AX099976.1  GI:13538986
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Sillaots,S., Martinez-Perez,A., Tsang,A. and Storms,R.
  TITLE     A multifunctional system for the efficient manipulation of protein
            expression in filamentous fungi and method using same
  JOURNAL   Patent: WO 0120007-A 5 22-MAR-2001;
            Concordia University (CA)
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FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        8 a      8 c      5 g      8 t
ORIGIN

  Query Match            71.1%;  Score 12.8;  DB 6;  Length 29;
  Best Local Similarity  87.5%;  Pred. No. 2.8e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 GAATGACGTTCCCTGT 17
          ||||||||| |||| |
Db      2 GAATGACGTCCCCTTT 17


RESULT 10
A16634
LOCUS       A16634                    50 bp    DNA     linear   PAT 04-OCT-1994
DEFINITION  Nucleotide sequence 9 from patent number EP0281530.
ACCESSION   A16634
VERSION     A16634.1  GI:641078
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Velati Bellini,A., Toma,S., Grandi,G., Colletti,E., Riboli,B.,
            Cosmina,P., Tognoni,A., Pedroni,P. and Rappuoli,R.
  TITLE     Recombinant plasmids useable for the expression of heterologous
            proteins in bacillus
  JOURNAL   Patent: EP 0281530-A 9 07-SEP-1988;
            ENIRICERCHE S.p.A.; SCLAVO S.p.A
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       11 a     12 c     15 g     12 t
ORIGIN

  Query Match            71.1%;  Score 12.8;  DB 6;  Length 50;
  Best Local Similarity  87.5%;  Pred. No. 2.7e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTG 16
          ||||||||| | ||||
Db      5 GGAATGACGATGCCTG 20


RESULT 11
A16645
LOCUS       A16645                    50 bp    DNA     linear   PAT 04-OCT-1994
DEFINITION  Nucleotide sequence 22 from patent number EP0281530.
ACCESSION   A16645
VERSION     A16645.1  GI:641088
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Velati Bellini,A., Toma,S., Grandi,G., Colletti,E., Riboli,B.,
            Cosmina,P., Tognoni,A., Pedroni,P. and Rappuoli,R.
  TITLE     Recombinant plasmids useable for the expression of heterologous
            proteins in bacillus
  JOURNAL   Patent: EP 0281530-A 22 07-SEP-1988;
            ENIRICERCHE S.p.A.; SCLAVO S.p.A
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       11 a     12 c     15 g     12 t
ORIGIN

  Query Match            71.1%;  Score 12.8;  DB 6;  Length 50;
  Best Local Similarity  87.5%;  Pred. No. 2.7e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTG 16
          ||||||||| | ||||
Db      5 GGAATGACGATGCCTG 20


RESULT 12
AX419077/c
LOCUS       AX419077                  26 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 96 from Patent WO0212471.
ACCESSION   AX419077
VERSION     AX419077.1  GI:21523851
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Acton,S., Robison,K.E. and Hsieh,F.Y.
  TITLE     Angiotensin converting enzyme homolog and uses therefor
  JOURNAL   Patent: WO 0212471-A 96 14-FEB-2002;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="motifs"
BASE COUNT        7 a      3 c      9 g      7 t
ORIGIN

  Query Match            68.9%;  Score 12.4;  DB 6;  Length 26;
  Best Local Similarity  92.9%;  Pred. No. 4.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GAATGACGTTCCCT 15
          ||||||| ||||||
Db     16 GAATGACTTTCCCT 3


RESULT 13
AX204048/c
LOCUS       AX204048                  51 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 154 from Patent WO0148245.
ACCESSION   AX204048
VERSION     AX204048.1  GI:15393526
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0148245-A 154 05-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg44000740"
BASE COUNT       16 a     15 c     13 g      7 t
ORIGIN

  Query Match            68.9%;  Score 12.4;  DB 6;  Length 51;
  Best Local Similarity  92.9%;  Pred. No. 4.6e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       5 TGACGTTCCCTGTG 18
           ||| ||||||||||
Db      39 TGATGTTCCCTGTG 26


RESULT 14
HSMYO7A55
LOCUS       HSMYO7A55                67 bp    DNA     linear   PRI 19-MAR-1997
DEFINITION  Human myosin VIIa (MYO7A) gene, 5' exon 38.
ACCESSION   U61467
VERSION     U61467.1  GI:1894878
KEYWORDS    .
SEGMENT     55 of 77
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 67)
  AUTHORS   Kelley,P.M., Weston,M.D., Chen,Z.-Y., Orten,D.J., Hasson,T.,
            Overbeck,L.D., Pinnti,J., Talmadge,C.B., Ing,P., Mooseker,M.S.,
            Corey,D., Sumegi,J. and Kimberling,W.J.
  TITLE     The genomic structure of the gene defective in Usher syndrome type
            Ib (MYO7A)
  JOURNAL   Genomics 40 (1), 73-79 (1997)
  MEDLINE   97224487
   PUBMED   9070921
REFERENCE   2  (bases 1 to 67)
  AUTHORS   Kelley,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUN-1996) Gene Marker Lab, Boys Town National
            Research Hospital, 555 North 30th Street, Omaha, NE 68131, USA
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     exon            42. .>67
                     /gene="MYO7A"
                     /number=38
BASE COUNT       11 a     24 c     21 g     11 t
ORIGIN

  Query Match            68.9%;  Score 12.4;  DB 9;  Length 67;
  Best Local Similarity  92.9%;  Pred. No. 4.5e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 TGACGTTCCCTGTG 18
           ||||| ||||||||
Db      19 TGACGGTCCCTGTG 32


RESULT 15
AR092212
LOCUS       AR092212                 70 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 150 from patent US 5998142.
ACCESSION   AR092212
VERSION     AR092212.1  GI:10018966
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Gold,L., Eaton,B., Smith,D., Wecker,M. and Jensen,K.
  TITLE     Systematic evolution of ligands by exponential enrichment:
            chemi-SELEX
  JOURNAL   Patent: US 5998142-A 150 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="unknown"
BASE COUNT       16 a     17 c     25 g     12 t
ORIGIN

  Query Match            68.9%;  Score 12.4;  DB 6;  Length 70;
  Best Local Similarity  92.9%;  Pred. No. 4.5e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 AATGACGTTCCCTG 16
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Db      34 AATGACGTACCCTG 47


Search completed: December 12, 2002, 02:55:28
Job time : 295.304 secs
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BASE COUNT
ORIGIN

Version 5.1.3
1993 - 2002 Compugen Ltd.

search, using sw model

December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
(without alignments)
1829.698 Million cell updates/sec

Title: US-09-355-254F-16
Perfect score: 20
Sequence: 1 gtccatttcccgtaaatctt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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13: gb_un:*
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15: em_ba:*
16: em_fun:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89795	A89795 Sequence 17
2		20	100.0	20	6	A90882	A90882 Sequence 17
3		20	100.0	20	6	AX455587	AX455587 Sequence
4		17.4	87.0	22	6	AX040434	AX040434 Sequence
5		17	85.0	19	6	I81948	I81948 Sequence 46
6		15.4	77.0	17	6	I87792	I87792 Sequence 20
7	c	15.4	77.0	19	6	I81949	I81949 Sequence 47
8	c	15.4	77.0	22	6	AX040435	AX040435 Sequence
9		15.4	77.0	25	6	AR182575	AR182575 Sequence
10		15.4	77.0	25	6	AX472568	AX472568 Sequence
11		15.4	77.0	25	6	AX476844	AX476844 Sequence
12		15.4	77.0	25	6	AX476862	AX476862 Sequence
13		15.4	77.0	28	6	I39727	I39727 Sequence 14
14		15.4	77.0	28	6	I55844	I55844 Sequence 14
15		15.2	76.0	20	6	AR103469	AR103469 Sequence
16		15.2	76.0	20	6	AR176473	AR176473 Sequence
17		14.4	72.0	18	6	AR153598	AR153598 Sequence
18	c	14.2	71.0	26	6	AR160395	AR160395 Sequence
19	c	14.2	71.0	26	6	AX482621	AX482621 Sequence
20		14.2	71.0	72	6	I95007	I95007 Sequence 24
21	c	14.2	71.0	76	6	I95006	I95006 Sequence 23
22		14	70.0	19	6	AX338646	AX338646 Sequence
23	c	13.8	69.0	25	6	AX192408	AX192408 Sequence
24	c	13.8	69.0	28	6	I39716	I39716 Sequence 3
25	c	13.8	69.0	28	6	I55833	I55833 Sequence 3
26	c	13.6	68.0	35	6	AR061506	AR061506 Sequence
27	c	13.6	68.0	35	6	AR108405	AR108405 Sequence
28	c	13.6	68.0	35	6	I16362	I16362 Sequence 18
29	c	13.6	68.0	35	6	I66848	I66848 Sequence 18
30	c	13.6	68.0	35	6	I84942	I84942 Sequence 18
31		13.6	68.0	94	11	AL773118	AL773118 Arabidops
32	c	13.2	66.0	66	10	MUSMUP	J00607 Mouse major
33		13.2	66.0	83	3	DME426807	AJ426807 Drosophil
34		13	65.0	13	6	AX026536	AX026536 Sequence
35		12.8	64.0	52	6	AR103470	AR103470 Sequence
36		12.8	64.0	52	6	AR176474	AR176474 Sequence
37		12.6	63.0	22	6	AR062163	AR062163 Sequence
38	c	12.6	63.0	30	6	AR004706	AR004706 Sequence
39	c	12.6	63.0	30	6	AR008192	AR008192 Sequence
40	c	12.6	63.0	30	6	AR136975	AR136975 Sequence
41	c	12.6	63.0	30	6	I76976	I76976 Sequence 36
42	c	12.6	63.0	30	6	I80971	I80971 Sequence 36
43	c	12.6	63.0	30	6	I81067	I81067 Sequence 36
44	c	12.6	63.0	46	6	AR126436	AR126436 Sequence
45		12.6	63.0	50	6	AR135509	AR135509 Sequence

ALIGNMENTS

RESULT 1
A89795
LOCUS A89795 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 17 from Patent WO9832462.
ACCESSION A89795
VERSION A89795.1 GI:6738309
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 17 30-JUL-1998;

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            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
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  Best Local Similarity  100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCATTTCCCGTAAATCTT 20
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Db      1 GTCCATTTCCCGTAAATCTT 20


RESULT 2
A90882
LOCUS       A90882                    20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 17 from Patent EP0855184.
ACCESSION   A90882
VERSION     A90882.1  GI:6739307
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 17 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      6 c      2 g      8 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCATTTCCCGTAAATCTT 20
          ||||||||||||||||||||
Db      1 GTCCATTTCCCGTAAATCTT 20


RESULT 3
AX455587
LOCUS       AX455587                  20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 64 from Patent WO0222809.
ACCESSION   AX455587
VERSION     AX455587.1  GI:21714655
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 64 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        4 a      6 c      2 g      8 t
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  Query Match            100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCCATTTCCCGTAAATCTT 20
          ||||||||||||||||||||
Db      1 GTCCATTTCCCGTAAATCTT 20


RESULT 4
AX040434
LOCUS       AX040434                  22 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 9 from Patent WO0063357.
ACCESSION   AX040434
VERSION     AX040434.1  GI:11230241
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Flier,J.S. and Bjorbaek,C.
  TITLE     Methods and compositions for modulating ciliary neurotrophic facto
            r activity
  JOURNAL   Patent: WO 0063357-A 9 26-OCT-2000;
            Beth Israel Deaconess Medical Center (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer-bind"
BASE COUNT        5 a      8 c      2 g      7 t
ORIGIN

  Query Match            87.0%;  Score 17.4;  DB 6;  Length 22;
  Best Local Similarity  94.7%;  Pred. No. 1.5e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 TCCATTTCCCGTAAATCTT 20
          |||||||||||||||||  |
Db      4 TCCATTTCCCGTAAATCAT 22


RESULT 5
I81948
LOCUS       I81948                    19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 46 from patent US 5712094.
ACCESSION   I81948
VERSION     I81948.1  GI:3210245
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
  TITLE     Methods for detecting modulators of cytokine action
  JOURNAL   Patent: US 5712094-A 46 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      6 c      2 g      6 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TCCATTTCCCGTAAATC 18
          |||||||||||||||||
Db      3 TCCATTTCCCGTAAATC 19


RESULT 6
I87792
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LOCUS       I87792                  17 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 20 from patent US 5716622.
ACCESSION   I87792
VERSION     I87792.1  GI:3407732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Darnell,J.E. Jr., Wen,Z., Horvath,C.M. and Zhong,Z.
  TITLE     Functionally active regions of signal transducer and activators of
            transcription
  JOURNAL   Patent: US 5716622-A 20 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      5 c      1 g      6 t
ORIGIN

  Query Match            77.0%;  Score 15.4;  DB 6;  Length 17;
  Best Local Similarity  94.1%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db      1 CATTTCCCGTAAATCAT 17


RESULT 7
I81949/c
LOCUS       I81949                  19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 47 from patent US 5712094.
ACCESSION   I81949
VERSION     I81949.1  GI:3210246
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
  TITLE     Methods for detecting modulators of cytokine action
  JOURNAL   Patent: US 5712094-A 47 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        6 a      2 c      6 g      5 t
ORIGIN

  Query Match            77.0%;  Score 15.4;  DB 6;  Length 19;
  Best Local Similarity  94.1%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db     19 CATTTCCCGTAAATCCT 3


RESULT 8
AX040435/c
LOCUS       AX040435                22 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 10 from Patent WO0063357.
ACCESSION   AX040435
VERSION     AX040435.1  GI:11230242
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Flier,J.S. and Bjorbaek,C.
  TITLE     Methods and compositions for modulating ciliary neurotrophic facto
            r activity
  JOURNAL   Patent: WO 0063357-A 10 26-OCT-2000;
            Beth Israel Deaconess Medical Center (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer-bind"
BASE COUNT        6 a      4 c      6 g      6 t
ORIGIN

  Query Match            77.0%;  Score 15.4;  DB 6;  Length 22;
  Best Local Similarity  94.1%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db     22 CATTTCCCGTAAATCAT 6


RESULT 9
AR182575
LOCUS       AR182575                25 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 23 from patent US 6338949.
ACCESSION   AR182575
VERSION     AR182575.1  GI:20225782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Darnell,J.E. Jr., Schindler,C.W., Fu,X.-Y., Wen,Z. and Zhong,Z.
  TITLE     Nucleic acids encoding receptor recognition factor stat4 and
            methods of use thereof
  JOURNAL   Patent: US 6338949-A 23 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .25
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BASE COUNT        6 a      7 c      5 g      7 t
ORIGIN

  Query Match            77.0%;  Score 15.4;  DB 6;  Length 25;
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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db      6 CATTTCCCGTAAATCGT 22


RESULT 10
AX472568
LOCUS       AX472568                25 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 63 from Patent WO02052039.
ACCESSION   AX472568
VERSION     AX472568.1  GI:22207472
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blais,Y., Rousseau,P., Leblanc,B. and Camato,R.N.
  TITLE     Methods for selecting and producing selective pharmaceutical
            compounds and compositions using an established genetically altered
            cell-based library responsive to transcription factors; genetic
            constructs and library therefor
  JOURNAL   Patent: WO 02052039-A 63 04-JUL-2002;
            Geneka Biotechnology Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .25
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BASE COUNT        6 a      7 c      5 g      7 t
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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db      6 CATTTCCCGTAAATCGT 22


RESULT 11
AX476844
LOCUS       AX476844                  25 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 21 from Patent WO02052037.
ACCESSION   AX476844
VERSION     AX476844.1  GI:22216120
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Larose,A.M., Rousseau,P., Leblanc,B. and Camato,R.
  TITLE     Method for screening and/or identifying factors that bind to
            nucleic acids
  JOURNAL   Patent: WO 02052037-A 21 04-JUL-2002;
            Geneka Biotechnology Inc. (CA)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="NABE-probes"
BASE COUNT        6 a      7 c      5 g      7 t
ORIGIN

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  Best Local Similarity   94.1%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db      6 CATTTCCCGTAAATCGT 22


RESULT 12
AX476862
LOCUS       AX476862                  25 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 39 from Patent WO02052037.
ACCESSION   AX476862
VERSION     AX476862.1  GI:22216138
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Larose,A.M., Rousseau,P., Leblanc,B. and Camato,R.
  TITLE     Method for screening and/or identifying factors that bind to
            nucleic acids
  JOURNAL   Patent: WO 02052037-A 39 04-JUL-2002;
            Geneka Biotechnology Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Double stranded NABE"
BASE COUNT        6 a      7 c      5 g      7 t
ORIGIN

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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 CATTTCCCGTAAATCTT 20
          ||||||||||||||| |
Db      6 CATTTCCCGTAAATCGT 22


RESULT 13
I39727
LOCUS       I39727                    28 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 14 from patent US 5616489.
ACCESSION   I39727
VERSION     I39727.1  GI:2084207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Levy,D.E.
  TITLE     DNA sequence which binds transcriptional regulatory proteins
            activated in response to various cytokines and uses thereof
  JOURNAL   Patent: US 5616489-A 14 01-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .28
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Qy      2 TCCATTTCCCGTAAATC 18
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Db      8 TTCATTTCCCGTAAATC 24


RESULT 14
I55844
LOCUS       I55844                    28 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 14 from patent US 5648217.
ACCESSION   I55844
VERSION     I55844.1  GI:2476638
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Levy,D.E.
  TITLE     DNA sequence which binds transcriptional regulatory proteins
            activated in response to various cytokines and uses thereof
  JOURNAL   Patent: US 5648217-A 14 15-JUL-1997;
FEATURES             Location/Qualifiers
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BASE COUNT        7 a      9 c      3 g      9 t
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Qy      2 TCCATTTCCCGTAAATC 18
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Db      8 TTCATTTCCCGTAAATC 24


RESULT 15
AR103469
LOCUS       AR103469                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6087478.
ACCESSION   AR103469
VERSION     AR103469.1  GI:12815057
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
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  AUTHORS   Vinkemeier,U., Moarefi,I., Darnell,J.E. Jr. and Kuriyan,J.
  TITLE     Crystal of the N-terminal domain of a STAT protein and methods of
            use thereof
  JOURNAL   Patent: US 6087478-A 5 11-JUL-2000;
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Search completed: December 12, 2002, 02:55:59
Job time : 323.116 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
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1829.698 Million cell updates/sec

Title: US-09-355-254F-17
Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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12: gb_sy:*
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14: gb_vi:*
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16: em_fun:*
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18: em_in:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
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26: em_ro:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89796	A89796 Sequence 18
2		20	100.0	20	6	A90883	A90883 Sequence 18
3		20	100.0	20	6	AX455591	AX455591 Sequence
4		19	95.0	24	6	AX406780	AX406780 Sequence
5		16	80.0	19	6	I79489	I79489 Sequence 75
6		16	80.0	19	6	I81942	I81942 Sequence 40
7		15	75.0	17	6	I87793	I87793 Sequence 21
8	c	15	75.0	19	6	I79490	I79490 Sequence 76
9	c	15	75.0	19	6	I81943	I81943 Sequence 41
10	c	14.8	74.0	47	6	AR032425	AR032425 Sequence
11	c	14.8	74.0	47	6	AR209089	AR209089 Sequence
12	c	14.8	74.0	47	6	I29165	I29165 Sequence 37
13	c	14.8	74.0	47	6	I90839	I90839 Sequence 37
14	c	14.8	74.0	50	6	AR032824	AR032824 Sequence
15	c	14.8	74.0	50	6	AR032825	AR032825 Sequence
16	c	14.8	74.0	50	6	AR209488	AR209488 Sequence
17	c	14.8	74.0	50	6	AR209489	AR209489 Sequence
18	c	14.8	74.0	50	6	I29564	I29564 Sequence 43
19	c	14.8	74.0	50	6	I29565	I29565 Sequence 43
20	c	14.8	74.0	50	6	I91238	I91238 Sequence 43
21	c	14.8	74.0	50	6	I91239	I91239 Sequence 43
22		14.4	72.0	19	6	I79437	I79437 Sequence 23
23		14.4	72.0	19	6	I79439	I79439 Sequence 25
24		14.4	72.0	19	6	I79447	I79447 Sequence 33
25		14.4	72.0	19	6	I79463	I79463 Sequence 49
26		14.4	72.0	19	6	I79465	I79465 Sequence 51
27		14.4	72.0	19	6	I79469	I79469 Sequence 55
28		14.4	72.0	19	6	I81944	I81944 Sequence 42
29		14.4	72.0	32	6	E09298	E09298 DNA linker.
30		13.6	68.0	50	6	E40770	E40770 Antihuman F
31	c	13.4	67.0	19	6	I79438	I79438 Sequence 24
32	c	13.4	67.0	19	6	I79440	I79440 Sequence 26
33	c	13.4	67.0	19	6	I79448	I79448 Sequence 34
34	c	13.4	67.0	19	6	I79464	I79464 Sequence 50
35	c	13.4	67.0	19	6	I79466	I79466 Sequence 52
36	c	13.4	67.0	19	6	I79470	I79470 Sequence 56
37	c	13.4	67.0	19	6	I81945	I81945 Sequence 43
38	c	13.4	67.0	24	6	AX444661	AX444661 Sequence
39	c	13.4	67.0	25	6	AX116799	AX116799 Sequence
40		13.4	67.0	51	6	AX163145	AX163145 Sequence
41		13.4	67.0	60	6	AR177644	AR177644 Sequence
42		13.4	67.0	93	9	AF281956	AF281956 Homo sapi
43		13.2	66.0	21	6	AX134134	AX134134 Sequence
44		13.2	66.0	21	6	AX189743	AX189743 Sequence
45		13.2	66.0	36	9	HUMALUAE	M62512 Human Alu r

ALIGNMENTS

RESULT 1
A89796
LOCUS A89796 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 18 from Patent WO9832462.
ACCESSION A89796
VERSION A89796.1 GI:6738310
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 18 30-JUL-1998;

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            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      3 c      4 g      8 t
ORIGIN

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Qy      1 TATGCATATTCCTGTAAGTG 20
          ||||||||||||||||||||
Db      1 TATGCATATTCCTGTAAGTG 20


RESULT 2
A90883
LOCUS       A90883                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 18 from Patent EP0855184.
ACCESSION   A90883
VERSION     A90883.1  GI:6739312
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 18 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      3 c      4 g      8 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAGTG 20
          ||||||||||||||||||||
Db      1 TATGCATATTCCTGTAAGTG 20


RESULT 3
AX455591
LOCUS       AX455591                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 68 from Patent WO0222809.
ACCESSION   AX455591
VERSION     AX455591.1  GI:21714659
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 68 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        5 a      3 c      4 g      8 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAGTG 20
          ||||||||||||||||||||
Db      1 TATGCATATTCCTGTAAGTG 20


RESULT 4
AX406780
LOCUS       AX406780                 24 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 36 from Patent WO0229044.
ACCESSION   AX406780
VERSION     AX406780.1  GI:21439705
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hecker,M. and Wagner,A.H.
  TITLE     Modulation of the transcription of pro-inflammatory gene products
  JOURNAL   Patent: WO 0229044-A 36 11-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"
BASE COUNT        6 a      4 c      4 g     10 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAGT 19
          |||||||||||||||||||
Db      6 TATGCATATTCCTGTAAGT 24


RESULT 5
I79489
LOCUS       I79489                   19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 75 from patent US 5707803.
ACCESSION   I79489
VERSION     I79489.1  GI:3207779
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lamb,I.Peter. and Seidel,H.Martin.
  TITLE     DNA regulatory elements responsive to cytokines and methods for
            their use
  JOURNAL   Patent: US 5707803-A 75 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      3 c      4 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 CATATTCCTGTAAGTG 20
          ||||||||||||||||
Db      4 CATATTCCTGTAAGTG 19


RESULT 6
I81942
LOCUS       I81942                   19 bp    DNA     linear   PAT 10-JUN-1998
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DEFINITION  Sequence 40 from patent US 5712094.
ACCESSION   I81942
VERSION     I81942.1  GI:3210239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
  TITLE     Methods for detecting modulators of cytokine action
  JOURNAL   Patent: US 5712094-A 40 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      3 c      4 g      7 t
ORIGIN

  Query Match            80.0%;  Score 16;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 CATATTCCTGTAAGTG 20
           ||||||||||||||||
Db       4 CATATTCCTGTAAGTG 19


RESULT 7
I87793
LOCUS       I87793                   17 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 21 from patent US 5716622.
ACCESSION   I87793
VERSION     I87793.1  GI:3407733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Darnell,J.E. Jr., Wen,Z., Horvath,C.M. and Zhong,Z.
  TITLE     Functionally active regions of signal transducer and activators of
            transcription
  JOURNAL   Patent: US 5716622-A 21 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      2 c      3 g      7 t
ORIGIN

  Query Match            75.0%;  Score 15;  DB 6;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1e+04;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ATATTCCTGTAAGTG 20
           |||||||||||||||
Db       1 ATATTCCTGTAAGTG 15


RESULT 8
I79490/c
LOCUS       I79490                   19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 76 from patent US 5707803.
ACCESSION   I79490
VERSION     I79490.1  GI:3207780
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lamb,I.Peter. and Seidel,H.Martin.
  TITLE     DNA regulatory elements responsive to cytokines and methods for
            their use
  JOURNAL   Patent: US 5707803-A 76 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        7 a      4 c      3 g      5 t
ORIGIN

  Query Match            75.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ATATTCCTGTAAGTG 20
           |||||||||||||||
Db      19 ATATTCCTGTAAGTG 5


RESULT 9
I81943/c
LOCUS       I81943                   19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 41 from patent US 5712094.
ACCESSION   I81943
VERSION     I81943.1  GI:3210240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
  TITLE     Methods for detecting modulators of cytokine action
  JOURNAL   Patent: US 5712094-A 41 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        7 a      4 c      3 g      5 t
ORIGIN

  Query Match            75.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ATATTCCTGTAAGTG 20
           |||||||||||||||
Db      19 ATATTCCTGTAAGTG 5


RESULT 10
AR032425/c
LOCUS       AR032425                 47 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 37 from patent US 5869241.
ACCESSION   AR032425
VERSION     AR032425.1  GI:5948030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Method of determining DNA sequence preference of a DNA-binding
            molecule
  JOURNAL   Patent: US 5869241-A 37 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       17 a      6 c     10 g     14 t
ORIGIN

  Query Match            74.0%;  Score 14.8;  DB 6;  Length 47;
  Best Local Similarity  88.9%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      28 TATTTATATTCCTGTAAG 11


RESULT 11
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AR209089/c
LOCUS       AR209089                47 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 37 from patent US 6384208.
ACCESSION   AR209089
VERSION     AR209089.1  GI:21510414
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence directed DNA binding molecules compositions and methods
  JOURNAL   Patent: US 6384208-A 37 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       17 a      6 c     10 g     14 t
ORIGIN

  Query Match             74.0%;  Score 14.8;  DB 6;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


RESULT 12
I29165/c
LOCUS       I29165                  47 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 37 from patent US 5578444.
ACCESSION   I29165
VERSION     I29165.1  GI:1819956
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence-directed DNA-binding molecules compositions and methods
  JOURNAL   Patent: US 5578444-A 37 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       17 a      6 c     10 g     14 t
ORIGIN

  Query Match             74.0%;  Score 14.8;  DB 6;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


RESULT 13
I90839/c
LOCUS       I90839                  47 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 37 from patent US 5726014.
ACCESSION   I90839
VERSION     I90839.1  GI:3935309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
  TITLE     Screening assay for the detection of DNA-binding molecules
  JOURNAL   Patent: US 5726014-A 37 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       17 a      6 c     10 g     14 t
ORIGIN

  Query Match             74.0%;  Score 14.8;  DB 6;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


RESULT 14
AR032824/c
LOCUS       AR032824                50 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 436 from patent US 5869241.
ACCESSION   AR032824
VERSION     AR032824.1  GI:5948429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Method of determining DNA sequence preference of a DNA-binding
            molecule
  JOURNAL   Patent: US 5869241-A 436 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       18 a      6 c     10 g     16 t
ORIGIN

  Query Match             74.0%;  Score 14.8;  DB 6;  Length 50;
  Best Local Similarity   88.9%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     32 TATTTATATTCCTGTAAG 15


RESULT 15
AR032825/c
LOCUS       AR032825                50 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 437 from patent US 5869241.
ACCESSION   AR032825
VERSION     AR032825.1  GI:5948430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Method of determining DNA sequence preference of a DNA-binding
            molecule
  JOURNAL   Patent: US 5869241-A 437 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       18 a      6 c     10 g     16 t
ORIGIN

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  Best Local Similarity   88.9%;  Pred. No. 1.1e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     32 TATTTATATTCCTGTAAG 15
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Job time : 321.116 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
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Title: US-09-355-254F-22
Perfect score: 20
Sequence: 1 aagcgaaaatgaaattgact 20

Scoring table: IDENTITY_NUC
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Searched: 2054640 seqs, 14551402878 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89801	A89801 Sequence 23
2		20	100.0	20	6	A90888	A90888 Sequence 23
3		20	100.0	20	6	AX455545	AX455545 Sequence
4		20	100.0	22	6	AX406763	AX406763 Sequence
5	c	20	100.0	22	6	AX406764	AX406764 Sequence
6	c	14.8	74.0	65	6	AX482985	AX482985 Sequence
7	c	14.4	72.0	21	6	AX392034	AX392034 Sequence
8		13.8	69.0	20	6	AR162873	AR162873 Sequence
9		13.8	69.0	20	6	AR194023	AR194023 Sequence
10	c	13.8	69.0	51	6	AX204090	AX204090 Sequence
11		13.6	68.0	24	6	AR174147	AR174147 Sequence
12	c	13.6	68.0	24	6	AX456503	AX456503 Sequence
13		13.6	68.0	50	6	AX060077	AX060077 Sequence
14	c	13.6	68.0	51	6	AX157392	AX157392 Sequence
15		13.6	68.0	89	9	HUMADPRT11	M29774 Human NAD+
16	c	13.4	67.0	25	6	AX488345	AX488345 Sequence
17	c	13.4	67.0	26	6	AX117947	AX117947 Sequence
18		13.2	66.0	30	6	AX023694	AX023694 Sequence
19		13.2	66.0	31	6	AR105818	AR105818 Sequence
20	c	13.2	66.0	35	6	AR049511	AR049511 Sequence
21	c	13.2	66.0	36	6	AR003843	AR003843 Sequence
22		13.2	66.0	65	6	AX485913	AX485913 Sequence
23		13.2	66.0	65	6	E02972	E02972 DNA encodin
24	c	13.2	66.0	94	6	AR140872	AR140872 Sequence
25	c	13.2	66.0	94	6	AR150822	AR150822 Sequence
26	c	13.2	66.0	94	6	I65700	I65700 Sequence 60
27	c	13.2	66.0	94	6	I67932	I67932 Sequence 60
28	c	13.2	66.0	94	6	I90153	I90153 Sequence 60
29		12.8	64.0	20	6	AR203176	AR203176 Sequence
30	c	12.8	64.0	24	6	AR034080	AR034080 Sequence
31	c	12.8	64.0	25	6	E04736	E04736 PCR primer.
32		12.8	64.0	27	6	AR099080	AR099080 Sequence
33		12.8	64.0	27	6	AR125428	AR125428 Sequence
34		12.8	64.0	27	6	AR127142	AR127142 Sequence
35		12.8	64.0	27	6	AR144700	AR144700 Sequence
36		12.8	64.0	27	6	AR151618	AR151618 Sequence
37	c	12.8	64.0	29	6	AR177299	AR177299 Sequence
38	c	12.8	64.0	29	6	BD003159	BD003159 Secretory
39	c	12.8	64.0	29	6	BD003183	BD003183 Secretory
40	c	12.8	64.0	29	6	I80078	I80078 Sequence 56
41		12.8	64.0	33	6	AR174978	AR174978 Sequence
42		12.8	64.0	33	6	AR208534	AR208534 Sequence
43		12.8	64.0	36	6	A38898	A38898 Sequence 6
44	c	12.8	64.0	36	6	A38899	A38899 Sequence 7
45		12.8	64.0	51	6	AX204531	AX204531 Sequence

ALIGNMENTS

RESULT 1
A89801
LOCUS A89801 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 23 from Patent WO9832462.
ACCESSION A89801
VERSION A89801.1 GI:6738315
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 23 30-JUL-1998;

```
            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       10 a      2 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||||||||||||||||||||
Db      1 AAGCGAAAATGAAATTGACT 20


RESULT 2
A90888
LOCUS       A90888                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 23 from Patent EP0855184.
ACCESSION   A90888
VERSION     A90888.1  GI:6739338
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 23 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       10 a      2 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||||||||||||||||||||
Db      1 AAGCGAAAATGAAATTGACT 20


RESULT 3
AX455545
LOCUS       AX455545                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 22 from Patent WO0222809.
ACCESSION   AX455545
VERSION     AX455545.1  GI:21714613
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 22 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT       10 a      2 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||||||||||||||||||||
Db      1 AAGCGAAAATGAAATTGACT 20


RESULT 4
AX406763
LOCUS       AX406763                 22 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 19 from Patent WO0229044.
ACCESSION   AX406763
VERSION     AX406763.1  GI:21439688
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hecker,M. and Wagner,A.H.
  TITLE     Modulation of the transcription of pro-inflammatory gene products
  JOURNAL   Patent: WO 0229044-A 19 11-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"
BASE COUNT       10 a      2 c      6 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||||||||||||||||||||
Db      3 AAGCGAAAATGAAATTGACT 22


RESULT 5
AX406764/c
LOCUS       AX406764                 22 bp    DNA     linear   PAT 15-JUN-2002
DEFINITION  Sequence 20 from Patent WO0229044.
ACCESSION   AX406764
VERSION     AX406764.1  GI:21439689
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hecker,M. and Wagner,A.H.
  TITLE     Modulation of the transcription of pro-inflammatory gene products
  JOURNAL   Patent: WO 0229044-A 20 11-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"
BASE COUNT        4 a      6 c      2 g     10 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||||||||||||||||||||
Db     20 AAGCGAAAATGAAATTGACT 1


RESULT 6
AX482985/c
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LOCUS       AX482985                65 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 285 from Patent WO02053728.
ACCESSION   AX482985
VERSION     AX482985.1  GI:22317405
KEYWORDS    .
SOURCE      Candida albicans.
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 285 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Candida albicans"
                     /db_xref="taxon:5476"
BASE COUNT       25 a      12 c       2 g      26 t
ORIGIN

  Query Match            74.0%;  Score 14.8;  DB 6;  Length 65;
  Best Local Similarity  88.9%;  Pred. No. 2.4e+04;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 AAGCGAAAATGAAATTGA 18
           ||  |||||||||||||||
Db      24 AAATGAAAATGAAATTGA 7


RESULT 7
AX392034/c
LOCUS       AX392034                21 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 24 from Patent WO0216613.
ACCESSION   AX392034
VERSION     AX392034.1  GI:19700541
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Matias Fonseca,S.C., Bald,A. and Soares Pais,M.S.
  TITLE     Pear genes codifying for _g(b)-galactosidase, pectin
            methylesterase, polygalacturonase, expansins and their use
  JOURNAL   Patent: WO 0216613-A 24 28-FEB-2002;
            Instituto de Ciencia Aplicada E Tecnologia (ICAT) (PT)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="specific primer"
     primer_bind     1. .21
BASE COUNT        4 a       5 c       4 g       8 t
ORIGIN

  Query Match            72.0%;  Score 14.4;  DB 6;  Length 21;
  Best Local Similarity  93.8%;  Pred. No. 3.8e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 CGAAAATGAAATTGAC 19
           |||||||||||| |||
Db      19 CGAAAATGAAATCGAC 4


RESULT 8
AR162873
LOCUS       AR162873                20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 13 from patent US 6258943.
ACCESSION   AR162873
VERSION     AR162873.1  GI:16230221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fong,T.Ming., Huang,R.-R.C. and Strader,C.D.
  TITLE     Human neurokinin-3 receptor
  JOURNAL   Patent: US 6258943-A 13 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        7 a       3 c       6 g       4 t
ORIGIN

  Query Match            69.0%;  Score 13.8;  DB 6;  Length 20;
  Best Local Similarity  88.2%;  Pred. No. 7e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 GCGAAAATGAAATTGAC 19
           ||| | ||||||||||||
Db       4 GCGTAGATGAAATTGAC 20


RESULT 9
AR194023
LOCUS       AR194023                20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 13 from patent US 6348330.
ACCESSION   AR194023
VERSION     AR194023.1  GI:20240615
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fong,T.Ming., Huang,R.-R.C. and Strader,C.D.
  TITLE     Method for measuring human neurokinin-3 receptor ligand binding
  JOURNAL   Patent: US 6348330-A 13 19-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        7 a       3 c       6 g       4 t
ORIGIN

  Query Match            69.0%;  Score 13.8;  DB 6;  Length 20;
  Best Local Similarity  88.2%;  Pred. No. 7e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 GCGAAAATGAAATTGAC 19
           ||| | ||||||||||||
Db       4 GCGTAGATGAAATTGAC 20


RESULT 10
AX204090/c
LOCUS       AX204090                51 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 196 from Patent WO0148245.
ACCESSION   AX204090
VERSION     AX204090.1  GI:15393579
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0148245-A 196 05-JUL-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg43119818"
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BASE COUNT       12 a     12 c     11 g     16 t
ORIGIN

  Query Match             69.0%;  Score 13.8;  DB 6;  Length 51;
  Best Local Similarity   88.2%;  Pred. No. 6.8e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 AGCGAAAATGAAATTGA 18
          || |||||||||| |||
Db     36 AGTGAAAATGAAACTGA 20


RESULT 11
AR174147
LOCUS       AR174147                 24 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 51 from patent US 6306636.
ACCESSION   AR174147
VERSION     AR174147.1  GI:17914467
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Haselkorn,R.H. and Gornicki,P.
  TITLE     Nucleic acid segments encoding wheat acetyl-CoA carboxylase
  JOURNAL   Patent: US 6306636-A 51 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        8 a      5 c      8 g      3 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 24;
  Best Local Similarity   80.0%;  Pred. No. 8.6e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||| | ||||| ||| ||||
Db      2 AAGGGGAAATGGAATCGACT 21


RESULT 12
AX456503/c
LOCUS       AX456503                 24 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 25 from Patent WO0227016.
ACCESSION   AX456503
VERSION     AX456503.1  GI:21715394
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Patel,S.B. and Dean,M.
  TITLE     Gene involved in dietary sterol absorption and excretion and uses
            therefor
  JOURNAL   Patent: WO 0227016-A 25 04-APR-2002;
            THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; Patel,
            Shailendra B. (US) ; Dean, Michael (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        4 a      4 c      2 g     14 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 24;
  Best Local Similarity   80.0%;  Pred. No. 8.6e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          || | |||||||||||  | |
Db     22 AAACAAAAAT@AAATTCAGT 3


RESULT 13
AX060077
LOCUS       AX060077                 50 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 14 from Patent WO0079008.
ACCESSION   AX060077
VERSION     AX060077.1  GI:12405718
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Kris,R.M. and Felder,S.
  TITLE     High throughput assay system
  JOURNAL   Patent: WO 0079008-A 14 28-DEC-2000;
            Kris, Richard M. (US) ; Felder, Stephen (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="linker"
BASE COUNT       16 a     11 c     14 g      9 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 50;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          ||  | |||||||||| ||
Db     11 AACTGGAAATGAAATTGGCT 30


RESULT 14
AX157392/c
LOCUS       AX157392                 51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 720 from Patent WO0140521.
ACCESSION   AX157392
VERSION     AX157392.1  GI:14538723
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 720 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="2 of 2 allelic variants (719 is other entry)
                     Accession number cg21150410"
BASE COUNT       15 a     12 c      9 g     15 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 51;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AAGCGAAAATGAAATTGACT 20
          | | ||| ||||| ||||||
Db     41 AGGAGAACATGAATTTGACT 22


RESULT 15
HUMADPRT11
LOCUS       HUMADPRT11               89 bp    DNA     linear   PRI 30-OCT-1994
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DEFINITION  Human NAD+ ADP-ribosyltransferase (ADPRT) gene, exon 11.
ACCESSION   M29774 M22953
VERSION     M29774.1  GI:178176
KEYWORDS    ADP-D-ribosyltransferase; NAD+ ADP-ribosyltransferase.
SEGMENT     11 of 23
SOURCE      Human HeLa cell line, cDNA to mRNA, clones Hz[19,20,21,22,23,24].
            and liver DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20; 70 to 89)
  AUTHORS   Auer,B., Nagl,U., Herzog,H., Schneider,R. and Schweiger,M.
  TITLE     Human nuclear NAD+ ADP-ribosyltransferase(polymerizing):
            organization of the gene
  JOURNAL   DNA 8 (8), 575-580 (1989)
  MEDLINE   90091744
   PUBMED   2513174
REFERENCE   2  (bases 11 to 79)
  AUTHORS   Herzog,H., Zabel,B.U., Schneider,R., Auer,B., Hirsch-Kauffmann,M.
            and Schweiger,M.
  TITLE     Human nuclear NAD+ ADP-ribosyltransferase: localization of the gene
            on chromosome 1q41-q42 and expression of an active human enzyme in
            Escherichia coli
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86 (10), 3514-3518 (1989)
  MEDLINE   89264454
   PUBMED   2498872
COMMENT     Draft entry and computer-readable sequence for [2] kindly submitted
            by H.Herzog, 07-MAR-1989.
FEATURES             Location/Qualifiers
     source          1. .89
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="1q41-q42"
     intron          <1. .10
                     /gene="PPOL"
                     /note="PPOL intron J"
     exon            11. .79
                     /gene="PPOL"
                     /note="NAD+ ADP-ribosyltransferase,  (EC 2.4.2.30; 5' end
                     put.); G00-119-508; putative"
                     /number=11
     intron          80. .>89
                     /gene="PPOL"
                     /note="PPOL intron K"
BASE COUNT       33 a     17 c     19 g     20 t
ORIGIN      About 0.6 kb after segment 10; chromosome 1q41-q42.

  Query Match             68.0%;  Score 13.6;  DB 9;  Length 89;
  Best Local Similarity   80.0%;  Pred. No. 8.1e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 AAGCGAAAATGAAATTGACT 20
           ||  || |||||||||  |||
Db      26 AAAAGAGAATGAAATTAACT 45


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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	19	AAV46001	Immune adjuvant IL
	2	18	100.0	18	24	AAL39185	Murine Toll-like r
	3	14.4	80.0	65	24	ABN30296	Rat spliced transc
c	4	13.8	76.7	38	15	AAQ57712	Proteoglycan core
c	5	13.8	76.7	89	24	ABK79561	Bacillus clausii g
	6	13.8	76.7	91	21	AAC21183	Human secreted pro
c	7	13.4	74.4	60	24	ABN37733	Human spliced tran
c	8	13.2	73.3	65	24	ABN29564	Rat spliced transc
	9	13.2	73.3	65	24	ABN58024	Mouse spliced tran
	10	13.2	73.3	65	24	ABN58058	Mouse spliced tra
c	11	13.2	73.3	90	22	AAK22893	Human brain expres
c	12	13.2	73.3	90	22	AAK49067	Human bone marrow
c	13	13.2	73.3	90	22	AAI54894	Probe #23580 used
c	14	13	72.2	28	19	AAV23036	HG3305S-28 primer
	15	12.8	71.1	29	22	AAF74984	E. nidulans PPyrG
	16	12.8	71.1	50	9	AAN81197	Pertussis S2 subun
	17	12.8	71.1	65	24	ABN29052	Rat spliced transc
	18	12.8	71.1	96	16	AAT19415	Human gene signatu
c	19	12.4	68.9	22	21	AAZ87493	Human ADH7 gene ex
c	20	12.4	68.9	26	24	AAD32654	Human ACE-2 DNA fr
c	21	12.4	68.9	51	22	AAH79539	Human DNA containi
c	22	12.4	68.9	60	24	ABN49023	Human spliced tran
	23	12.4	68.9	70	17	AAT97765	Nucleic acid inhib
	24	12.4	68.9	70	21	AAZ52674	High salt SELEX hu
	25	12.4	68.9	72	16	AAT21588	Human gene signatu
	26	12.4	68.9	85	24	ABK15932	Human lung tumour
	27	12.2	67.8	24	19	AAV09031	Human hH1 sodium c
	28	12.2	67.8	30	24	ABK11663	Rabbit calreticuli
	29	12.2	67.8	33	15	AAQ63125	Extension motif fo
c	30	12.2	67.8	41	24	ABL50365	Human ribosomal pr
c	31	12.2	67.8	41	24	ABL50366	Human ribosomal pr
	32	12.2	67.8	50	23	ABL01010	Human SNP involvin
c	33	12.2	67.8	51	23	ABL00204	Human silent nonco
c	34	12.2	67.8	65	24	ABN28425	Rat spliced transc
c	35	12	66.7	33	19	AAV54224	Murine T-cell rece
c	36	12	66.7	33	19	AAV54228	Primer KC117 used
c	37	12	66.7	33	20	AAX55310	Soluble sc-TCR fus
c	38	12	66.7	33	20	AAX55306	Soluble sc-TCR fus
	39	12	66.7	56	16	AAQ86442	FIPV SM protein DN
c	40	12	66.7	56	22	AAH43094	PCR primer used to
	41	12	66.7	77	22	ABA70510	Human foetal liver
	42	12	66.7	77	22	ABA37136	Probe #15602 for g
	43	12	66.7	77	22	AAK18755	Human brain expres
	44	12	66.7	77	22	AAK44691	Human bone marrow
	45	12	66.7	77	22	AAI24978	Probe #14911 for g

ALIGNMENTS

RESULT 1
AAV46001
ID AAV46001 standard; DNA; 18 BP.
XX
AC AAV46001;
XX
DT 16-OCT-1998 (first entry)
XX
DE Immune adjuvant IL-13.
XX
KW Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;
KW modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;
KW Ig class; autoimmune response; T-cell; B-cell; tumour; ss.
XX
OS Class Bacteria.
XX
PN EP855184-A1.
XX
PD 29-JUL-1998.
XX
PF 23-JAN-1997; 97EP-0101019.
XX
PR 23-JAN-1997; 97EP-0101019.
XX
PA (HEEG/) HEEG K.
PA (LIPF/) LIPFORD G B.
PA (WAGN/) WAGNER H.
XX
PI Heeg K, Lipford GB, Wagner H;
XX
DR WPI; 1998-389630/34.
XX

PT Antigenic composition comprises polynucleotide fragment and antigen
PT - used as vaccine to treat or prevent e.g. cancer or pathogen
PT infections and to modulate immune response e.g. tolerance break and
PT regulation of TH1/TH2 cells
XX
PS Example 5; Page 8; 28pp; English.
XX
CC AAV45993-V46019 are fragments of bacterial polynucleotides which are
CC used as immune adjuvants for inclusion into vaccines to treat cancer and
CC for prophylaxis and/or treatment of conditions caused by pathogenic
CC micro-organisms. The polynucleotide is used for modulation of an immune
CC response and the modulation is selected from the group break of
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig
CC classes, treatment of autoimmune responses and induction of tolerances.
CC DNA oligomers are used to enhance the reactivity of immune cells to
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination
CC against tumour-defined antigens and immunostimulatory substances in an
CC immune response against tumours and to suppress immune reactions of the
CC innate and acquired immune system. The composition is inexpensive and
CC stable and does not cause lethal shock, which happens with prior art
CC bacterial sequences.
XX
SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAATGACGTTCCCTGTG 18
||||||||||||||||||
Db 1 GGAATGACGTTCCCTGTG 18

RESULT 2
AAL39185
ID AAL39185 standard; DNA; 18 BP.
XX
AC AAL39185;
XX
DT 05-SEP-2002 (first entry)
XX
DE Murine Toll-like receptor related CpG DNA SEQ ID No 60.
XX
KW Murine Toll-like receptor; TLR9; TLR7; TLR8; ISNA; ds.
XX
OS Unidentified.
XX
PN WO200222809-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US29229.
XX
PR 15-SEP-2000; 2000US-233035P.
PR 23-JAN-2001; 2001US-263657P.
PR 17-MAY-2001; 2001US-291726P.
PR 22-JUN-2001; 2001US-300210P.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Bauer S, Lipford G, Wagner H;
XX
DR WPI; 2002-393964/42.
XX
PT New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides,
PT useful for identifying species specificity of immunostimulatory nucleic
PT acid and identifying immunostimulatory nucleic acids -
XX
PS Disclosure; Page 76; 195pp; English.
XX
CC The invention relates to isolated murine Toll-like receptors (TLR)9,
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The
CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC TLR7, TLR8 and TLR9 polypeptides are also useful for comparing TLR9
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide
CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention.
XX
SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAATGACGTTCCCTGTG 18
||||||||||||||||||
Db 1 GGAATGACGTTCCCTGTG 18

RESULT 3
ABN30296
ID ABN30296 standard; DNA; 65 BP.
XX
AC ABN30296;
XX
DT 15-JUL-2002 (first entry)
XX
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:3044.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 3044; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 BP; 18 A; 13 C; 16 G; 18 T; 0 other;

Query Match 80.0%; Score 14.4; DB 24; Length 65;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AATGACGTTCCCTGTG 18
||||||||||||||| |
Db 9 AATGACGTTCCCTGCG 24

RESULT 4
AAQ57712/c
ID AAQ57712 standard; DNA; 38 BP.
XX
AC AAQ57712;
XX
DT 11-AUG-1994 (first entry)
XX
DE Proteoglycan core glycoprotein antisense primer.
XX
KW Neurocan; cell adhesion; leukocyte-endothelial cell recognition; lipid;
KW tissue-related inflammation allergy; cellular; humoural; carbohydrate;
KW hypersensitivity; trauma; neuronal development; cell transport; enzyme;
KW infection; diagnosis; lectin; versican; aggrecan; gelsolin; saccharide;
KW receptor; cell recognition; membrane cytoplasmic protein; nucleoside;
KW ion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 28
FT /*tag= a
FT /label= Inosine
XX
PN WO9403601-A.
XX
PD 17-FEB-1994.
XX
PF 03-AUG-1993; 93WO-US07306.
XX
PR 03-AUG-1992; 92US-0922911.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Margolis RK, Margolis RU, Rauch U;
XX
DR WPI; 1994-065690/08.
XX
PT Eukaryotic neurocan polypeptide(s) with epidermal growth factor,
PT lectin or complement binding activity - used in the diagnosis,
PT treatment or research of hypersensitivity and allergic diseases
XX
PS Example 1; Fig 1B; 105pp; English.
XX
CC The sequences given in AAQ57711-12 represent primers which were used
CC for the isolation of the neurocan cDNA. The neurocan protein
CC has several biological activities, including cell adhesion, leukocyte-
CC endothelial cell recognition, tissue-related inflammation allergies,
CC cellular and/or humoural hypersensitivity, trauma, neuronal
CC development, and cell transport and/or infection. Compositions
CC containing them can be used as modulators of these conditions, and
CC may be used as therapeutic, diagnostic, and/or research tools.
CC Neurocan peptides can be used to mimic proteins, such as lectins,
CC cell adhesion molecules, versicans, aggrecans or gelsolins, as
CC receptor or effector subtypes. The protein can be used to treat
CC diseases involving a qualitative or quantitative pathological
CC abnormality of cell adhesion or leukocyte-endothelial cell recognition,
CC or a functionally associated molecule such as a membrane cytoplasmic
CC protein, lipid, carbohydrate, saccharide, nucleoside, enzyme or ion.
XX
SQ Sequence 38 BP; 7 A; 9 C; 5 G; 10 T; 7 other;

Query Match 76.7%; Score 13.8; DB 15; Length 38;
Best Local Similarity 70.6%; Pred. No. 5.2e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAATGACGTTCCCTGT 17
||||:||:|| || ||:
Db 38 GGAAYGAYGTNCCNTGY 22

RESULT 5
ABK79561/c
ID ABK79561 standard; DNA; 89 BP.
XX
AC ABK79561;
XX
DT 13-AUG-2002 (first entry)
XX
DE Bacillus clausii genomic sequence tag (GST) #2404.
XX
KW Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
OS Bacillus clausii.
XX
PN WO200229113-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US31437.
XX
PR 06-OCT-2000; 2000US-0680598.
PR 27-MAR-2001; 2001US-279526P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX
PI Berka R, Clausen IG;
XX
DR WPI; 2002-416684/44.
XX
PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second
PT Bacillus cells, by using substrate containing Bacillus genomic
PT sequenced tag array -
XX
PS Claim 11; SEQ ID NO 6852; 200pp; English.
XX
CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of

```
CC   genes in a first Bacillus cell relative to expression of the same genes
CC   in one or more second Bacillus cells. The method is useful for monitoring
CC   global expression of several genes from a Bacillus cell, discovering new
CC   genes, identifying possible functions of unknown open reading frames and
CC   monitoring gene copy number variation and stability. Monitoring changes
CC   in expression of genes may be used to provide a representation of the way
CC   in which Bacillus cells adapt to changes in culture conditions,
CC   environmental stress or other physiological provocation. Extensive
CC   follow-up characterisation is unnecessary, when one spot on an array
CC   equals one gene or one open reading frame, since sequence information is
CC   available. This sequence represents a genomic sequence tag (GST) used in
CC   the method of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 89 BP; 21 A; 16 C; 29 G; 23 T; 0 other;

  Query Match             76.7%;  Score 13.8;  DB 24;  Length 89;
  Best Local Similarity   88.2%;  Pred. No. 5.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GAATGACGTTCCCTGTG 18
           ||| ||| |||||||||
Db      88 GAAAGACATTCCCTGTG 72


RESULT 6
AAC21183
ID   AAC21183 standard; cDNA; 91 BP.
XX
AC   AAC21183;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 25258.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 25258; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 91 BP; 36 A; 15 C; 17 G; 22 T; 1 other;

  Query Match             76.7%;  Score 13.8;  DB 21;  Length 91;
  Best Local Similarity   88.2%;  Pred. No. 5.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GAATGACGTTCCCTGTG 18
           |||| | ||||||||||
Db      43 GAATCATGTTCCCTGTG 59


RESULT 7
ABN37733/c
ID   ABN37733 standard; DNA; 60 BP.
XX
AC   ABN37733;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:10481.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB01903.
XX
PR   28-JUL-2000; 2000US-221607P.
PR   02-MAY-2001; 2001US-287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of
PT   a genome, useful for detecting tissue-, pathology-, and
PT   developmental-specific genes  -
XX
PS   Example 1; SEQ ID 10481; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the
CC   (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises
CC   several oligonucleotides, each capable of hybridising selectively to a
CC   set of messenger RNAs transcribed from a given transcription unit of
CC   the genome, which encodes one or more messenger RNA splice variants.
CC   The oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a
CC   particular biological or pathological state, and so allowing the
CC   detection of tissue- and pathology-specific genes such as those genes
CC   only expressed in specific tissue under a specific pathological
CC   condition; to detect developmental specific genes; and to detect RNA
CC   transcripts and splice variants of a transcriptome of a patient suffering
CC   from a particular disorder. ABN27253 to ABN59589 represent
CC   oligonucleotide sequences from rats, humans and mice, which are used in
```

CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 18 A; 5 C; 20 G; 17 T; 0 other;

Query Match 74.4%; Score 13.4; DB 24; Length 60;
Best Local Similarity 93.3%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AATGACGTTCCCTGT 17
||| ||||||||||
Db 38 AATCACGTTCCCTGT 24

RESULT 8
ABN29564/c
ID ABN29564 standard; DNA; 65 BP.
XX
AC ABN29564;
XX
DT 15-JUL-2002 (first entry)
XX
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2312.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 2312; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in

CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 BP; 20 A; 17 C; 16 G; 12 T; 0 other;

Query Match 73.3%; Score 13.2; DB 24; Length 65;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAATGACGTTCCCTGTG 18
|||||| | |||| ||||
Db 29 GGAATGTCCTTCCATGTG 12

RESULT 9
ABN58024
ID ABN58024 standard; DNA; 65 BP.
XX
AC ABN58024;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:30772.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 30772; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in

```
CC   the exemplification of the present invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC , specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 65 BP; 15 A; 20 C; 19 G; 11 T; 0 other;

  Query Match             73.3%;  Score 13.2;  DB 24;  Length 65;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          |||| ||||  |||||||
Db     43 GGAAGGACGCACCCTGTG 60


RESULT 10
ABN58058
ID   ABN58058 standard; DNA; 65 BP.
XX
AC   ABN58058;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Mouse spliced transcript detection oligonucleotide SEQ ID NO:30806.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss..
XX
OS   Mus musculus.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB01903.
XX
PR   28-JUL-2000; 2000US-221607P.
PR   02-MAY-2001; 2001US-287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of
PT   a genome, useful for detecting tissue-, pathology-, and
PT   developmental-specific genes -
XX
PS   Example 1; SEQ ID 30806; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the
CC   (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises
CC   several oligonucleotides, each capable of hybridising selectively to a
CC   set of messenger RNAs transcribed from a given transcription unit of
CC   the genome, which encodes one or more messenger RNA splice variants.
CC   The oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a
CC   particular biological or pathological state, and so allowing the
CC   detection of tissue- and pathology-specific genes such as those genes
CC   only expressed in specific tissue under a specific pathological
CC   condition; to detect developmental specific genes; and to detect RNA
CC   transcripts and splice variants of a transcriptome of a patient suffering
CC   from a particular disorder. ABN27253 to ABN59589 represent
CC   oligonucleotide sequences from rats, humans and mice, which are used in
CC   the exemplification of the present invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 65 BP; 20 A; 17 C; 15 G; 13 T; 0 other;

  Query Match             73.3%;  Score 13.2;  DB 24;  Length 65;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          ||||||| | | ||||||
Db     15 GGAATGAAGGTTCCTGTG 32


RESULT 11
AAK22893/c
ID   AAK22893 standard; DNA; 90 BP.
XX
AC   AAK22893;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 22884.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 22884; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 90 BP; 18 A; 33 C; 15 G; 24 T; 0 other;

  Query Match             73.3%;  Score 13.2;  DB 22;  Length 90;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          |||| || | ||||||||
```

```
Db     68 GGAAAGAAGCTCCCTGTG 51


RESULT 12
AAK49067/c
ID   AAK49067 standard; DNA; 90 BP.
XX
AC   AAK49067;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 23624.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00668.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human bone marrow -
XX
PS   Example 4; SEQ ID NO: 23624; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention.
XX
SQ   Sequence 90 BP; 18 A; 33 C; 15 G; 24 T; 0 other;

  Query Match             73.3%;  Score 13.2;  DB 22;  Length 90;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          |||| || | ||||||||
Db     68 GGAAAGAAGCTCCCTGTG 51


RESULT 13
AAI54894/c
ID   AAI54894 standard; DNA; 90 BP.
XX
AC   AAI54894;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Probe #23580 used to measure gene expression in human placenta sample.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
XX
PS   Claim 25; SEQ ID No 23580; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
XX
SQ   Sequence 90 BP; 18 A; 33 C; 15 G; 24 T; 0 other;

  Query Match             73.3%;  Score 13.2;  DB 22;  Length 90;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GGAATGACGTTCCCTGTG 18
          |||| || | ||||||||
Db     68 GGAAAGAAGCTCCCTGTG 51


RESULT 14
AAV23036/c
ID   AAV23036 standard; DNA; 28 BP.
XX
AC   AAV23036;
XX
DT   30-JUL-1998  (first entry)
XX
DE   HG3305S-28 primer used to amplify Hepatitis virus g gene sequences.
XX
KW   Hepatitis g virus gene; diagnosis; treatment; Hepatitis g virus disease;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Hepatitis g virus.
XX
PN   JP10108685-A.
XX
PD   28-APR-1998.
XX
PF   10-AUG-1997;   97JP-0227387.
XX
PR   10-AUG-1996;   96JP-0227639.
XX
PA   (BMLB-) BML KK.
XX
DR   WPI; 1998-304974/27.
XX
```

PT New hepatitis G virus gene - useful for diagnosing and treating
PT diseases caused by virus
XX
PS Disclosure; Page 6; 128pp; Japanese.
XX
CC PCR primers AAV23018-74 were used to amplify and isolate new Hepatitis g
CC virus gene (see AAV23075-83 for gene fragments). RNA was synthesised
CC from the serum of nine patients judged positive for Hepatitis g virus
CC and cDNA synthesised from this RNA. The cDNA was used as a template in
CC several PCR reactions to isolate fragments of the new gene. The gene
CC may be useful for diagnosing and developing treatments for Hepatitis g
CC virus diseases.
XX
SQ Sequence 28 BP; 8 A; 8 C; 5 G; 7 T; 0 other;

Query Match 72.2%; Score 13; DB 19; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ATGACGTTCCCTG 16
||||||||||||
Db 28 ATGACGTTCCCTG 16

RESULT 15
AAF74984
ID AAF74984 standard; DNA; 29 BP.
XX
AC AAF74984;
XX
DT 23-MAY-2001 (first entry)
XX
DE E. nidulans PPyrG sense primer PPyr3'.
XX
KW GlaA; promoter; PyrG; PkiA; LacA; terminator; PCR primer; adapter;
KW protein expression; filamentous fungus; Escherichia coli;
KW Aspergillus niger; expression vector; ss.
XX
OS Emericella nidulans.
XX
PN WO200120007-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-CA01084.
XX
PR 13-SEP-1999; 99US-0153228.
XX
PA (UYCO-) UNIV CONCORDIA.
XX
PI Sillaots S, Martinez-Perez A, Tsang A, Storms R;
XX
DR WPI; 2001-244813/25.
XX
PT Expression vector for isolating filamentous fungi that expresses a
PT protein of interest at high levels, has selectable marker for fungi and
PT promoter operably linked to nucleic acid sequence encoding the protein
PT -
XX
PS Example 3; Page 33; 54pp; English.
XX
CC The present invention describes an expression vector (I) capable of
CC enabling a systematic analysis of gene expression and/or high-throughput
CC strain improvement screens in filamentous fungi, comprising a selectable
CC marker for the filamentous fungi and a promoter operably linked to a
CC sequence encoding a protein of interest or its part. Also described is a
CC filamentous fungi strain (II), enabling the expression of a protein of
CC interest to greater than 100, preferably greater than 1000 times
CC compared to the level in a parent strain. (I) is useful for isolating a
CC filamentous fungi, in particular Aspergillus niger that expresses a
CC protein of interest at high levels required for industrial-scale protein
CC production. (I) increases the expression of the protein of interest by
CC 100 times, preferably 1000 times, as compared to the level of expression
CC in a control filamentous fungi strain. (I) increases the efficiency and
CC reduces the time required for isolating strains that express proteins of
CC interest at high levels. AAF74980 to AAF74997 represent oligonucleotide
CC sequences used in an example from the present invention.
XX
SQ Sequence 29 BP; 8 A; 8 C; 5 G; 8 T; 0 other;

Query Match 71.1%; Score 12.8; DB 22; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAATGACGTTCCCTGT 17
||||||||| |||| |
Db 2 GAATGACGTCCCCTTT 17

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Job time : 96.087 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
(without alignments)
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Perfect score: 20
Sequence: 1 caggcataacggttccgtag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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15: em_ba:*
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23: em_pat:*
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27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	6	A89802	A89802 Sequence 24
2	20	100.0	20	6	A90889	A90889 Sequence 24
3	20	100.0	20	6	AX455564	AX455564 Sequence
c 4	15.2	76.0	25	6	AX196810	AX196810 Sequence
5	13.6	68.0	24	6	AX445605	AX445605 Sequence
6	13.4	67.0	31	6	BD002472	BD002472 Gene comp
c 7	13	65.0	20	6	E07207	E07207 PCR primer
8	12.8	64.0	33	6	AX262268	AX262268 Sequence
9	12.8	64.0	35	6	AX262303	AX262303 Sequence
10	12.8	64.0	39	6	AX262285	AX262285 Sequence
c 11	12.8	64.0	65	6	AX486035	AX486035 Sequence
c 12	12.8	64.0	97	6	I44826	I44826 Sequence 1
c 13	12.6	63.0	33	6	A32217	A32217 Synthetic m
c 14	12.6	63.0	50	6	AX103395	AX103395 Sequence
15	12.2	61.0	30	6	AX374961	AX374961 Sequence
16	12.2	61.0	31	6	AR106260	AR106260 Sequence
17	12.2	61.0	31	6	E61282	E61282 Method for
c 18	12.2	61.0	37	6	AR145069	AR145069 Sequence
c 19	12.2	61.0	37	6	AR168079	AR168079 Sequence
c 20	12.2	61.0	37	6	AR169792	AR169792 Sequence
c 21	12.2	61.0	37	6	AR204850	AR204850 Sequence
c 22	12	60.0	33	6	A48801	A48801 Sequence 2
c 23	12	60.0	36	6	AX247485	AX247485 Sequence
c 24	12	60.0	39	6	AX052711	AX052711 Sequence
25	12	60.0	51	6	AX159959	AX159959 Sequence
26	12	60.0	63	6	AX482092	AX482092 Sequence
c 27	12	60.0	72	9	HSU91302	U91302 Homo sapien
c 28	12	60.0	90	9	HSCLCHX13	Z25758 Homo sapien
29	11.8	59.0	24	6	AX445387	AX445387 Sequence
c 30	11.8	59.0	26	6	AR125091	AR125091 Sequence
31	11.8	59.0	31	6	BD002473	BD002473 Gene comp
32	11.8	59.0	33	6	AR008899	AR008899 Sequence
33	11.8	59.0	33	6	AR087594	AR087594 Sequence
34	11.8	59.0	35	6	A84225	A84225 Sequence 4
c 35	11.8	59.0	38	6	AR038218	AR038218 Sequence
36	11.8	59.0	39	6	AX080158	AX080158 Sequence
37	11.8	59.0	61	6	AX080156	AX080156 Sequence
38	11.8	59.0	65	6	AX484924	AX484924 Sequence
c 39	11.8	59.0	100	14	S82444	S82444 {3' region,
c 40	11.8	59.0	100	14	S82445	S82445 {3' region,
c 41	11.8	59.0	100	14	S82446	S82446 {3' region,
42	11.6	58.0	24	6	AX443631	AX443631 Sequence
43	11.6	58.0	25	6	AX447613	AX447613 Sequence
c 44	11.6	58.0	28	6	AR160111	AR160111 Sequence
c 45	11.6	58.0	35	6	AR084174	AR084174 Sequence

ALIGNMENTS

RESULT 1
A89802
LOCUS A89802 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 24 from Patent WO9832462.
ACCESSION A89802
VERSION A89802.1 GI:6738316
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 24 30-JUL-1998;

```
          LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      6 g      4 t
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 9.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCGTAG 20
          ||||||||||||||||||||
Db      1 CAGGCATAACGGTTCCGTAG 20


RESULT 2
A90889
LOCUS       A90889                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 24 from Patent EP0855184.
ACCESSION   A90889
VERSION     A90889.1  GI:6739343
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 24 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      6 g      4 t
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 9.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCGTAG 20
          ||||||||||||||||||||
Db      1 CAGGCATAACGGTTCCGTAG 20


RESULT 3
AX455564
LOCUS       AX455564                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 41 from Patent WO0222809.
ACCESSION   AX455564
VERSION     AX455564.1  GI:21714632
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 41 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        5 a      5 c      6 g      4 t
ORIGIN
```

```
  Query Match            100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 9.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCGTAG 20
          ||||||||||||||||||||
Db      1 CAGGCATAACGGTTCCGTAG 20


RESULT 4
AX196810/c
LOCUS       AX196810                 25 bp    DNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 517 from Patent WO0151627.
ACCESSION   AX196810
VERSION     AX196810.1  GI:15387016
KEYWORDS    .
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
  TITLE     Nucleic acid molecules and other molecules associated with soybean
            cyst nematode resistance
  JOURNAL   Patent: WO 0151627-A 517 19-JUL-2001;
            MONSANTO COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /note="Seq ID: 240017_region_G3__6395_12_Forward_Primer"
BASE COUNT        6 a      6 c      6 g      7 t
ORIGIN

  Query Match             76.0%;  Score 15.2;  DB 6;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCGTAG 20
          ||||||  ||||||| ||||
Db     22 CAGGCACCACGGTTCAGTAG 3


RESULT 5
AX445605
LOCUS       AX445605                 24 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 2060 from Patent WO0216649.
ACCESSION   AX445605
VERSION     AX445605.1  GI:21692886
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gunderson,K.
  TITLE     Probes and decoder oligonucleotides
  JOURNAL   Patent: WO 0216649-A 2060 28-FEB-2002;
            Illumina, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Computer Generated Probe Sequence."
BASE COUNT        6 a      5 c      9 g      4 t
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 24;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCGTAG 20
```

```
          ||||||| || ||  |||||
Db      2 CAGGCATGACAGTGGCGTAG 21


RESULT 6
BD002472
LOCUS       BD002472                  31 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene composition and method.
ACCESSION   BD002472
VERSION     BD002472.1  GI:18630433
KEYWORDS    JP 2000245487-A/138.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Sha,N., Walinton,J. and Patel,N.
  TITLE     Gene composition and method
  JOURNAL   Patent: JP 2000245487-A 138 12-SEP-2000;
            AFIMETRICS INC
COMMENT     OS   Unknown
            PN   JP 2000245487-A/138
            PD   12-SEP-2000
            PF   27-JAN-2000 JP 2000019392
            PR   27-JAN-1999 US   09/238.402
            PI   NIRA SHA,JANET WALINTON,NIRA PATEL
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .31
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .31
                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT       10 a      6 c      5 g      9 t      1 others
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 31;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+04;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCG 17
          |:|||| ||| ||||||
Db     15 CRGGCAAAACTGTTCCG 31


RESULT 7
E07207/c
LOCUS       E07207                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer to detect Acholeplasma sp.
ACCESSION   E07207
VERSION     E07207.1  GI:2175348
KEYWORDS    JP 1994098800-A/2.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Nakagawa,T., Uemori,T., Asada,K., Katou,I. and Harasawa,A.
  TITLE     METHOD FOR DETECTING ACHOLEPLASMA
  JOURNAL   Patent: JP 1994098800-A 2 12-APR-1994;
            TAKARA SHUZO CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994098800-A/2
            PD   12-APR-1994
            PF   21-SEP-1992 JP 1992274830
            PI   NAKAGAWA TOMOKO, UEMORI TAKASHI, ASADA KIYOZOU, PI   KATOU
            IKUNOSHIN,
            PI   HARASAWA AKIRA
            PC   C12Q1/68,C12Q1/68,C12N15/11,C12Q1/04,(C12Q1/04,C12R1:01); CC
            strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT        4 a      7 c      3 g      4 t      2 others
ORIGIN

  Query Match             65.0%;  Score 13;  DB 6;  Length 20;
  Best Local Similarity   76.5%;  Pred. No. 5.4e+04;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 GCATAACGGTTCCGTAG 20
          | || |||||||:|||:
Db     18 GGATCACGGTTCSGTAR 2


RESULT 8
AX262268
LOCUS       AX262268                  33 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 24 from Patent WO0173052.
ACCESSION   AX262268
VERSION     AX262268.1  GI:16511217
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mchenry,C.S.
  TITLE     Thermophilic polymerase III holoenzyme
  JOURNAL   Patent: WO 0173052-A 24 04-OCT-2001;
            McHenry, Charles S. (US)
FEATURES              Location/Qualifiers
     source           1. .33
                      /organism="synthetic construct"
                      /db_xref="taxon:32630"
                      /note="ATG forward primer P118-S85"
BASE COUNT       13 a      10 c      5 g      5 t
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 6;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 6.8e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      5 CATAACGGTTCCGTAG 20
          ||||||||||||  ||
Db     11 CATAACGGTTCCCAAG 26


RESULT 9
AX262303
LOCUS       AX262303                  35 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 59 from Patent WO0173052.
ACCESSION   AX262303
VERSION     AX262303.1  GI:16511248
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mchenry,C.S.
  TITLE     Thermophilic polymerase III holoenzyme
  JOURNAL   Patent: WO 0173052-A 59 04-OCT-2001;
            McHenry, Charles S. (US)
FEATURES              Location/Qualifiers
     source           1. .35
                      /organism="synthetic construct"
                      /db_xref="taxon:32630"
                      /note="forward/sense ATG primer P118-S78cla2"
BASE COUNT       15 a      7 c      6 g      7 t
ORIGIN
```

```
  Query Match            64.0%;  Score 12.8;  DB 6;  Length 35;
  Best Local Similarity  87.5%;  Pred. No. 6.8e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      5 CATAACGGTTCCGTAG 20
          ||||||||||||  ||
Db     17 CATAACGGTTCCCAAG 32


RESULT 10
AX262285
LOCUS       AX262285                  39 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 41 from Patent WO0173052.
ACCESSION   AX262285
VERSION     AX262285.1  GI:16511230
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mchenry,C.S.
  TITLE     Thermophilic polymerase III holoenzyme
  JOURNAL   Patent: WO 0173052-A 41 04-OCT-2001;
            McHenry, Charles S. (US)
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ATG primer P118-S74"
BASE COUNT       15 a      9 c      7 g      8 t
ORIGIN

  Query Match            64.0%;  Score 12.8;  DB 6;  Length 39;
  Best Local Similarity  87.5%;  Pred. No. 6.8e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      5 CATAACGGTTCCGTAG 20
          ||||||||||||  ||
Db     21 CATAACGGTTCCCAAG 36


RESULT 11
AX486035/c
LOCUS       AX486035                  65 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 3335 from Patent WO02053728.
ACCESSION   AX486035
VERSION     AX486035.1  GI:22320251
KEYWORDS    .
SOURCE      Candida albicans.
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 3335 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Candida albicans"
                     /db_xref="taxon:5476"
BASE COUNT       18 a      10 c      11 g      26 t
ORIGIN

  Query Match            64.0%;  Score 12.8;  DB 6;  Length 65;
  Best Local Similarity  87.5%;  Pred. No. 6.7e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCC 16
          ||| ||||||||| |||
Db     61 CAGTCATAACGGATCC 46


RESULT 12
I44826/c
LOCUS       I44826                    97 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5635601.
ACCESSION   I44826
VERSION     I44826.1  GI:2469539
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 97)
  AUTHORS   Moyle,M. and McLean,J.W.
  TITLE     Beta-8 integrin subunit antibodies
  JOURNAL   Patent: US 5635601-A 1 03-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .97
                     /organism="unknown"
BASE COUNT       26 a      18 c      33 g      20 t
ORIGIN

  Query Match            64.0%;  Score 12.8;  DB 6;  Length 97;
  Best Local Similarity  87.5%;  Pred. No. 6.7e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 GGCATAACGGTTCCGT 18
          |||||  |||||||||
Db     30 GGCATCTCGGTTCCGT 15


RESULT 13
A32217/c
LOCUS       A32217                    33 bp    DNA     linear   PAT 03-JUL-1996
DEFINITION  Synthetic mutagenic primer.
ACCESSION   A32217
VERSION     A32217.1  GI:1567327
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      10 c      7 g      11 t
ORIGIN

  Query Match            63.0%;  Score 12.6;  DB 6;  Length 33;
  Best Local Similarity  78.9%;  Pred. No. 8.8e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CAGGCATAACGGTTCCGTA 19
          |||   |||||| ||||||
Db     28 CAGAAGTAACGGATCCGTA 10


RESULT 14
AX103395/c
LOCUS       AX103395                  50 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 17 from Patent EP1104813.
ACCESSION   AX103395
VERSION     AX103395.1  GI:13919680
KEYWORDS    .
SOURCE      unidentified adenovirus.
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Rademaker,H.J., Fallaux,F.J., de Jong,R.N., van der Vliet,P.C. and
            Hoeben,R.C.
  TITLE     Conditional replication of recombinant human adenovirus dna
            carrying modified inverted terminal repeat sequences
  JOURNAL   Patent: EP 1104813-A 17 06-JUN-2001;
            Leids Universitair Medisch Centrum (NL)
```

```
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unidentified adenovirus"
                     /db_xref="taxon:10535"
     misc_feature    1. .50
                     /note="'BAd'"
BASE COUNT       15 a      10 c      10 g      15 t
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 6;  Length 50;
  Best Local Similarity   78.9%;  Pred. No. 8.7e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CAGGCATAACGGTTCCGTA 19
           || ||| ||  ||||||||
Db      33 CACGCAAAAGTGTTCCGTA 15


RESULT 15
AX374961
LOCUS       AX374961                 30 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 14 from Patent WO0210425.
ACCESSION   AX374961
VERSION     AX374961.1  GI:19169806
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Porro,D. and Sauer,M.
  TITLE     Ascorbic acid production from yeasts
  JOURNAL   Patent: WO 0210425-A 14 07-FEB-2002;
            Biopolo S.C.A.R.L. (IT)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Forward PCR Primer for L-galactono-1,4-lactone
                     dehydrogenase from A. thaliana"
BASE COUNT        8 a       9 c       6 g       7 t
ORIGIN

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 30;
  Best Local Similarity   82.4%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 AGGCATAACGGTTCCGT 18
           |||| |||  |||||||
Db       6 AGGCCTAAATGTTCCGT 22


Search completed: December 12, 2002, 02:56:25
Job time : 324.116 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:04:50 ; Search time 102.319 Seconds
(without alignments)
440.192 Million cell updates/sec

Title: US-09-355-254F-8
Perfect score: 20
Sequence: 1 gattgcctgacgtcagagag 20

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	19	AAV46000	Immune adjuvant AP
	2	20	100.0	20	20	AAZ28189	Chlamydia trachoma
	3	20	100.0	20	21	AAZ99172	Inflammatory cardi
	4	20	100.0	20	24	AAL39177	Murine Toll-like r
	5	20	100.0	26	20	AAX76047	cAMP response elem
	6	20	100.0	27	18	AAT85832	CRE oligonucloide
	7	20	100.0	27	20	AAV82454	ATF comp oligonucl
	8	20	100.0	27	20	AAV08336	CRE element coding
	9	20	100.0	27	22	AAI70581	Transcription fact
	10	20	100.0	27	22	AAH77396	Cyclic AMP respons
c	11	20	100.0	27	22	AAH77397	Cyclic AMP respons
	12	20	100.0	27	22	AAF87956	Cyclic-AMP respons
c	13	20	100.0	27	22	AAF87957	Cyclic-AMP respons
	14	20	100.0	27	22	AAF76267	cAMP response elem
	15	20	100.0	27	24	ABA92274	CRE binding site o
	16	20	100.0	27	24	ABA05538	Cyclic-AMP respons
	17	19	95.0	20	19	AAV45997	Immune adjuvant CR
	18	16.4	82.0	28	24	ABK14052	Cyclic AMP respons
	19	16.4	82.0	32	22	AAF77813	CREB probe derived
	20	16.4	82.0	37	19	AAV04084	Somatostatin gene
	21	16.4	82.0	50	15	AAQ69701	Human somatostatin
	22	16.4	82.0	50	18	AAT64163	Human somatostatin
	23	16.4	82.0	50	20	AAX17451	Test sequence from
	24	16.4	82.0	50	24	ABK82942	DNA binding molecu
	25	15.8	79.0	20	19	AAV45999	Immune adjuvant CR
c	26	14.8	74.0	95	21	AAC30099	Human secreted pro
	27	14.4	72.0	33	24	ABK87820	Somatostatin promo
c	28	14.4	72.0	33	24	ABK87821	Somatostatin promo
	29	14.4	72.0	83	24	AAS98555	Human Pleckstrin h
c	30	14.2	71.0	41	19	AAV50622	Brassica sp. polym
c	31	14.2	71.0	41	24	ABL96051	Brassica polymorph
c	32	14.2	71.0	60	24	ABN49177	Human spliced tran
c	33	13.8	69.0	65	24	ABN57982	Mouse spliced tran
c	34	13.6	68.0	51	22	AAI78809	Human silent SNP c
c	35	13.4	67.0	96	21	AAC12454	Human secreted pro
	36	13.2	66.0	22	19	AAV04086	PEPCK gene cAMP re
	37	13.2	66.0	25	22	AAH39807	SNP specific SNPE
	38	13.2	66.0	47	21	AAZ69295	Human map-related
	39	13.2	66.0	51	22	AAH39808	Human SNP flanking
	40	13.2	66.0	60	24	ABN45698	Human spliced tran
	41	13.2	66.0	62	22	AAI66152	Hepatitis E virus
	42	13.2	66.0	65	24	ABN56672	Mouse spliced tran
	43	13.2	66.0	90	24	ABK36416	HIV DNA encoding N
c	44	13	65.0	26	19	AAV46019	Immune adjuvant CR
	45	12.8	64.0	21	19	AAV41019	Primer PLZFRARA:12

ALIGNMENTS

RESULT 1
AAV46000
ID AAV46000 standard; DNA; 20 BP.
XX
AC AAV46000;
XX
DT 16-OCT-1998 (first entry)
XX
DE Immune adjuvant AP-1 #1.
XX
KW Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;
KW modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;
KW Ig class; autoimmune response; T-cell; B-cell; tumour; ss.
XX
OS Class Bacteria.
XX
PN EP855184-A1.
XX
PD 29-JUL-1998.
XX
PF 23-JAN-1997; 97EP-0101019.
XX
PR 23-JAN-1997; 97EP-0101019.
XX
PA (HEEG/) HEEG K.
PA (LIPF/) LIPFORD G B.
PA (WAGN/) WAGNER H.
XX
PI Heeg K, Lipford GB, Wagner H;
XX
DR WPI; 1998-389630/34.
XX

PT Antigenic composition comprises polynucleotide fragment and antigen
PT - used as vaccine to treat or prevent e.g. cancer or pathogen
PT infections and to modulate immune response e.g. tolerance break and
PT regulation of TH1/TH2 cells
XX
PS Example 3; Page 7; 28pp; English.
XX
CC AAV45993-V46019 are fragments of bacterial polynucleotides which are
CC used as immune adjuvants for inclusion into vaccines to treat cancer and
CC for prophylaxis and/or treatment of conditions caused by pathogenic
CC micro-organisms. The polynucleotide is used for modulation of an immune
CC response and the modulation is selected from the group break of
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig
CC classes, treatment of autoimmune responses and induction of tolerances.
CC DNA oligomers are used to enhance the reactivity of immune cells to
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination
CC against tumour-defined antigens and immunostimulatory substances in an
CC immune response against tumours and to suppress immune reactions of the
CC innate and acquired immune system. The composition is inexpensive and
CC stable and does not cause lethal shock, which happens with prior art
CC bacterial sequences.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTGCCTGACGTCAGAGAG 20
||||||||||||||||||||
Db 1 GATTGCCTGACGTCAGAGAG 20

RESULT 2
AAZ28189
ID AAZ28189 standard; DNA; 20 BP.
XX
AC AAZ28189;
XX
DT 20-DEC-1999 (first entry)
XX
DE Chlamydia trachomatis outer membrane protein gene-derived CpG oligo 2.
XX
KW Heart disease; inflammatory; autoimmune; cardiomyopathy; adjuvant;
KW CpG motif; vaccine; ds.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = phosphorothioate linkage"
XX
PN US5962636-A.
XX
PD 05-OCT-1999.
XX
PF 12-AUG-1998; 98US-0133774.
XX
PR 12-AUG-1998; 98US-0133774.
XX
PA (AMGE-) AMGEN CANADA INC.
XX
PI Bachmaier K, Hessel AJ, Penninger JM, Neu N;
XX
DR WPI; 1999-589735/50.
XX
PT Peptides that induce or suppress inflammatory cardiomyopathy -
XX
PS Example 2; Column 25; 17pp; English.
XX
CC This sequence represents DNA encoding Chlamydia trachomatis 60 kD outer
CC membrane protein (OMP) gene-derived CpG oligonucleotide 2. This
CC oligonucleotide contains a CpG motif. It was tested for its ability to
CC act as an adjuvant for the M7A-alpha peptide (AAY42723), which can
CC induce inflammatory cardiomyopathy (ICM) in mice. It was found to act as
CC a potent immunostimulator, whereas a oligonucleotide from the same
CC source which did not contain a CpG motif (AAZ28193) was hardly effective
CC as an adjuvant. Inflammatory cardiomyopathy peptides (AAY42723,
CC AAY42725-Y42731) can be used with such an adjuvant and an excipient in a
CC vaccine for decreasing ICM.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTGCCTGACGTCAGAGAG 20
||||||||||||||||||||
Db 1 GATTGCCTGACGTCAGAGAG 20

RESULT 3
AAZ99172
ID AAZ99172 standard; DNA; 20 BP.
XX
AC AAZ99172;
XX
DT 21-JUN-2000 (first entry)
XX
DE Inflammatory cardiomyopathy immunostimulatory oligonucleotide #1.
XX
KW Cardiant; murine alpha myosin heavy chain; inflammatory myocarditis;
KW autoimmune inflammatory cardiomyopathy; Chlamydia; antibody; vaccine;
KW hybridization probe; immunostimulatory; ss.
XX
OS Synthetic.
XX
PN US6034230-A.
XX
PD 07-MAR-2000.
XX
PF 03-MAY-1999; 99US-0303862.
XX
PR 12-AUG-1998; 98US-0133774.
XX
PA (AMGE-) AMGEN CANADA INC.
XX
PI Neu N, Penninger JM, Bachmaier K, Hessel AJ;
XX
DR WPI; 2000-255712/22.
XX
PT DNA molecules encoding novel myocardial peptides used for inhibiting
PT and inducing inflammatory cardiomyopathy in vivo -
XX
PS Disclosure; Column 17; 17pp; English.
XX
CC The invention relates to the isolation of sequences coding for peptide
CC sequences derived from bacteria and viruses which may cause inflammatory
CC cardiomyopathy. The peptide sequences are searched based on the sequence
CC of the M7A peptides derived from the murine alpha myosin heavy chain
CC polypeptide. The consensus sequence of the murine M7A-alpha/beta peptides
CC (Y83813) was used to search the PIR public database for similar bacterial
CC and viral sequences able to cause inflammatory cardiomyopathy. The screen
CC isolated the peptides Y83814-Y83819 and their corresponding coding
CC sequences Z99164-Z99169. The peptides encoded by the DNAs are used, alone
CC or in conjunction with other therapeutics, for inducing or inhibiting
CC inflammatory cardiomyopathy in vivo, where the cardiomyopathy is
CC autoimmune inflammatory cardiomyopathy, and inflammatory cardiomyopathy
CC caused by Chlamydia or other bacterial or viral infections that cause
CC inflammatory cardiomyopathy. The oligonucleotides Z99172-Z99176 were
CC shown to increase the immunogenicity of the immunostimulatory peptides

CC when injected simultaneously. The peptides may also be used for
CC increasing inflammatory myocarditis in a mammal. Antibodies against the
CC peptides and the peptides themselves are used for measuring the risk of
CC inflammatory cardiomyopathy in a mammal. The peptides may also be used
CC in vaccines. Nucleic acids encoding the peptides may be used as
CC hybridization probes, e.g. in diagnostic assays to test for the
CC presence of Chlamydia DNA.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTGCCTGACGTCAGAGAG 20
||||||||||||||||||||
Db 1 GATTGCCTGACGTCAGAGAG 20

RESULT 4
AAL39177
ID AAL39177 standard; DNA; 20 BP.
XX
AC AAL39177;
XX
DT 05-SEP-2002 (first entry)
XX
DE Murine Toll-like receptor related CpG DNA SEQ ID No 52.
XX
KW Murine Toll-like receptor; TLR9; TLR7; TLR8; ISNA; ds.
XX
OS Unidentified.
XX
PN WO200222809-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US29229.
XX
PR 15-SEP-2000; 2000US-233035P.
PR 23-JAN-2001; 2001US-263657P.
PR 17-MAY-2001; 2001US-291726P.
PR 22-JUN-2001; 2001US-300210P.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Bauer S, Lipford G, Wagner H;
XX
DR WPI; 2002-393964/42.
XX
PT New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides,
PT useful for identifying species specificity of immunostimulatory nucleic
PT acid and identifying immunostimulatory nucleic acids -
XX
PS Disclosure; Page 76; 195pp; English.
XX
CC The invention relates to isolated murine Toll-like receptors (TLR)9,
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The
CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC TLR7, TLR8 and TLR9 polypeptides are also useful for comparing TLR9
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide
CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTGCCTGACGTCAGAGAG 20
||||||||||||||||||||
Db 1 GATTGCCTGACGTCAGAGAG 20

RESULT 5
AAX76047
ID AAX76047 standard; DNA; 26 BP.
XX
AC AAX76047;
XX
DT 30-JUL-1999 (first entry)
XX
DE cAMP response element oligonucleotide SEQ ID NO:15.
XX
KW CRE; cAMP response element; transcription factor decoy; cis-element;
KW tumour growth inhibitor; palindrome; hairpin; cancer; metabolism;
KW gene transcription regulation; inhibiting proliferation; ds.
XX
OS Synthetic.
XX
PN WO9926634-A1.
XX
PD 03-JUN-1999.
XX
PF 23-NOV-1998; 98WO-US25307.
XX
PR 24-NOV-1997; 97US-0977643.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Cho-Chung YS;
XX
DR WPI; 1999-347612/29.
XX
PT Nucleic acids that compete with response elements for transcription
PT factors
XX
PS Example 10; Page 54; 83pp; English.
XX
CC The present invention describes a composition (A) comprising one or more
CC nucleic acids (I) that compete with cAMP (cyclic adenosine monophosphate)
CC response element (CRE) enhancer DNA for binding to transcription factors
CC (TF). (I) are used to regulate gene transcription in cells, in vitro or
CC in vivo, specifically for inhibiting proliferation of cancer cells, but
CC possibly also for regulation of metabolism in hepatitis B and other
CC viruses. HCT-15 human multidrug resistant colon carcinoma cells (2
CC million) were inoculated subcutaneously into the flank of nude mice,
CC then the CRE oligonucleotide 5'-TGACGTTCATGACGTTCATGACGTTCA-3' injected
CC intraperitoneally at doses of 0.1 mg, 5 times per week, once the tumour
CC had reached 30-50 mg. This treatment resulted in over 85% reduction in
CC tumour growth, relative to an untreated control. (I) have high affinity
CC for TF and can inhibit growth of cancer cells without adverse effects on
CC normal cells (contrast use of antisense RNA). The method does not
CC require knowledge of the target gene sequence, only of the response
CC element sequence. The present sequence is used in the exemplification
CC of the present invention.
XX
SQ Sequence 26 BP; 8 A; 4 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 6
AAT85832
ID   AAT85832 standard; DNA; 27 BP.
XX
AC   AAT85832;
XX
DT   21-NOV-1997  (first entry)
XX
DE   CRE oligonucloide used in gel shift assay.
XX
KW   Activating transcription factor 1; ATF1; CREB; recognition sequence;
KW   cyclic AMP responsive element binding protein; inhibition; binding;
KW   proliferation; virus; cancer; HTLV1; leukaemia; antibody; ss.
XX
OS   Synthetic.
XX
PN   US5641486-A.
XX
PD   24-JUN-1997.
XX
PF   18-MAR-1994;   94US-0210880.
XX
PR   18-MAR-1994;   94US-0210880.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Hinrichs SH,  Orten DJ;
XX
DR   WPI; 1997-340900/31.
XX
PT   Inhibiting replication of cancer cells or viruses - with inhibitor
PT   that binds to peptide sequence of activating transcription factor 1
XX
PS   Example 2; Column 6; 17pp; English.
XX
CC   This oligonucleotide sequence corresponds to the cyclic AMP binding
CC   element (CRE) to which members of the activating transcription factor 1
CC   (ATF1)-cyclic AMP responsive element binding protein (CREB) family
CC   of protein bind.  The sequence was used in a gel shift mobility assay to
CC   identify agents which inhibit the binding of ATF1 to its recognition
CC   sequence.  The agents are preferably antibodies, small molecules or
CC   polypeptides, especially the complementarity determining region of
CC   monoclonal antibody MAb4.  The agents cause inhibition of transcription
CC   by dissociating ATF1 from its target gene and thus will prevent
CC   proliferation of e.g. a virus or cancer cell, such as HTLV1-mediated
CC   leukaemic cell proliferation.
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 18;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 7
AAV82454
ID   AAV82454 standard; DNA; 27 BP.
XX
AC   AAV82454;
XX
DT   12-APR-1999  (first entry)
XX
DE   ATF comp oligonucleotide used in competition analysis.
XX
KW   Vascular endothelial growth factor; VEGF; human; hypoxia;
KW   vascular disease; tumour; cancer; angiogenesis; wound healing;
KW   therapy; diagnosis; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9856936-A1.
XX
PD   17-DEC-1998.
XX
PF   10-JUN-1998;   98WO-EP03517.
XX
PR   10-JUN-1997;   97EP-0109418.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Damert A,  Plate K,  Risau W;
XX
DR   WPI; 1999-080911/07.
XX
PT   New recombinant DNA - contains sequence that regulates
PT   hypoxia-induced expression, used for, e.g. treatment and diagnosis
PT   of vascular disease
XX
PS   Example 6; Page 41; 80pp; English.
XX
CC   Oligonucleotides hVEGF, hVEGF 5' DEL, AP1M1 and AP1M2 (see
CC   AAV82449-52), and competitor oligonucleotides AP1 comp, ATF comp
CC   and VL30 (see AAV82453-55) were used in electrophoretic mobility
CC   shift assays to determing which transcription factor(s) bind to
CC   the cis-acting element that is involved in the potentiation of
CC   hypoxia inducible factor 1 (HIF-1) mediated hypoxic induction
CC   of vascular endothelial growth factor (VEGF) gene regulatory
CC   sequences.  Experiments were performed using normoxic or hypoxic
CC   C6 cell nuclear extracts.  An AP1 consensus binding site was shown
CC   to compete for DNA-protein-complex formation at potentiating
CC   sequences.  The invention relates to recombinant DNA molecules
CC   comprising regulatory sequences of the VEGF gene, especially the
CC   3' untranslated region (see AAV82439) and promoter (see AAV82440),
CC   being capable of modulating hypoxia inducible expression of a
CC   heterologous DNA in vivo.  Such recombinant DNA molecules, vectors,
CC   host cells and transgenic animals can be used to identify and
CC   develop compounds and methods for diagnosing, treating, preventing
CC   and/or delaying a vascular or tumour disease.
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 20;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 8
AAV08336
ID   AAV08336 standard; DNA; 27 BP.
XX
AC   AAV08336;
XX
DT   04-FEB-1999  (first entry)
XX
DE   CRE element coding sequence.
XX
KW   ATF1; activating transcription factor 1; inhibitor; gene transcription;
KW   cell proliferation; cancer cell; human; ds.
XX
OS   Synthetic.
XX
PN   US5844096-A.
```

```
XX
PD   01-DEC-1998.
XX
PF   20-DEC-1996;   96US-0771411.
XX
PR   18-MAR-1994;   94US-0210880.
PR   20-DEC-1996;   96US-0771411.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Hinrichs SH,  Orten DJ;
XX
DR   WPI; 1999-044667/04.
XX
PT   Inhibitor of activating transcription factor 1 mediated gene
PT   transcription - useful as anticancer or antiviral agent
XX
PS   Example 2; Column 6; 17pp; English.
XX
CC   This sequence represents a CRE element coding sequence. This sequence
CC   was used to test the effect of the inhibitory compound of the
CC   invention. The inhibitory compound binds to ATF1 residues 167-181 with
CC   sufficient affinity to dissociate AFT1 from a gene to which it is bound
CC   and thereby prevent transcription of the gene. The inhibitory compound
CC   and its derivatives are useful for inhibiting the ATF1-mediated
CC   proliferation of cancer cells and viruses, e.g. HTLV I.
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 20;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.5;.
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 9
AAI70581
ID   AAI70581 standard; DNA; 27 BP.
XX
AC   AAI70581;
XX
DT   21-JAN-2002  (first entry)
XX
DE   Transcription factor CREB consensus oligonucleotide.
XX
KW   Transcription factor; CREB; screening; detection; quantification;
KW   probe; ds.
XX
OS   Synthetic.
XX
PN   EP1136567-A1.
XX
PD   26-SEP-2001.
XX
PF   24-MAR-2000; 2000EP-0870057.
XX
PR   24-MAR-2000; 2000EP-0870057.
XX
PA   (ADAR-) ADVANCED ARRAY TECHNOLOGIES SA.
XX
PI   Remacle J,  Renard P,  Art M;
XX
DR   WPI; 2001-640391/74.
XX
PT   Screening, detecting or quantifying transcriptional factors in a
PT   biological sample comprises contacting the transcriptional factor with
PT   a double-stranded DNA sequence bound to an insoluble solid support  -
XX
PS   Example 4; Page 8; 20pp; English.
XX
CC   The present sequence is that of a CREB transcription factor
CC   consensus oligonucleotide.  Double-stranded probe nucleotide
CC   sequences were constructed from 100 bp of a CMV 5' sequence (see
CC   AAI70578) linked to this oligonucleotide and used in microwell
CC   colorimetric CREB and phospho-CREB assays.  The double-stranded
CC   probe was biotinylated at its CMV 5' extremity and linked to
CC   streptavidin-coated 96-wells plates.  The plates were contacted
CC   with a nuclear extract of L929 murine fibrosarcoma cells,
CC   incubated with anti-CREB or anti-phospho-CREB antibody and then
CC   with peroxidase-conjugated antibody.  The presence of CREB or
CC   phospho-CREB was detected through the action of peroxidase on
CC   tetramethylbenzidine.  This is an example of the method of the
CC   invention, involving the detection of a transcription factor using
CC   a double-stranded DNA probe bound to an insoluble solid support at
CC   a concentration of at least 0.01 pmole/sq cm of support surface and
CC   at a distance of at least 6.8 nm from the surface of the support.
CC   The method allows the screening, detection and/or quantification of
CC   one or more transcriptional factors, of molecules binding such
CC   factors, and of molecules that inhibit such binding, using
CC   non-radioactive detection methods.
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 10
AAH77396
ID   AAH77396 standard; DNA; 27 BP.
XX
AC   AAH77396;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Cyclic AMP response element CRE consensus oligonucleotide probe #1.
XX
KW   Cancer; human; dithiocarbamate derivative; anticancer agent; probe; ss.
XX
OS   Unidentified.
XX
PN   US2001016600-A1.
XX
PD   23-AUG-2001.
XX
PF   12-DEC-2000; 2000US-0735205.
XX
PR   08-SEP-1998;   98US-0099390.
PR   08-SEP-1999;   99US-0392122.
PR   05-OCT-2000; 2000US-0679932.
XX
PA   (KENN/) KENNEDY T P.
XX
PI   Kennedy TP;
XX
DR   WPI; 2001-557127/62.
XX
PT   Treating cancer, asthma and cancer and reducing hypoxic or ischemic
PT   damage comprises administering dithiocarbamate thiolate anion or
PT   dithiocarbamate thiolate metal complex -
XX
PS   Disclosure; Page 10; 36pp; English.
XX
CC   The present invention describes a method of treating cancer, asthma and
CC   arthritis and reducing hypoxic or ischaemic damage, involving
CC   administering a dithiocarbamate thiolate anion or metal ion complex to
CC   the patient. The present sequence is a probe for the cyclic AMP response
CC   element CRE, which was described in the exemplification of the invention.
```

```
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 11
AAH77397/c
ID   AAH77397 standard; DNA; 27 BP.
XX
AC   AAH77397;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Cyclic AMP response element CRE consensus oligonucleotide probe #2.
XX
KW   Cancer; human; dithiocarbamate derivative; anticancer agent; probe; ss.
XX
OS   Unidentified.
XX
PN   US2001016600-A1.
XX
PD   23-AUG-2001.
XX
PF   12-DEC-2000; 2000US-0735205.
XX
PR   08-SEP-1998;   98US-0099390.
PR   08-SEP-1999;   99US-0392122.
PR   05-OCT-2000; 2000US-0679932.
XX
PA   (KENN/) KENNEDY T P.
XX
PI   Kennedy TP;
XX
DR   WPI; 2001-557127/62.
XX
PT   Treating cancer, asthma and cancer and reducing hypoxic or ischemic
PT   damage comprises administering dithiocarbamate thiolate anion or
PT   dithiocarbamate thiolate metal complex -
XX
PS   Disclosure; Page 10; 36pp; English.
XX
CC   The present invention describes a method of treating cancer, asthma and
CC   arthritis and reducing hypoxic or ischaemic damage, involving
CC   administering a dithiocarbamate thiolate anion or metal ion complex to
CC   the patient. The present sequence is a probe for the cyclic AMP response
CC   element CRE, which was described in the exemplification of the invention.
XX
SQ   Sequence 27 BP; 5 A; 9 C; 5 G; 8 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db     24 GATTGCCTGACGTCAGAGAG 5


RESULT 12
AAF87956
ID   AAF87956 standard; DNA; 27 BP.
XX
AC   AAF87956;
XX
DT   20-JUL-2001  (first entry)
XX
DE   Cyclic-AMP responsive element CRE consensus oligo for EMSA #1.
XX
KW   Cyclic-AMP responsive element; electrophoretic mobility shift assay;
KW   EMSA; CRE; NF-kappaB; cancer; tetraethyl thiuram disulphide;
KW   dithiocarbamate; tumour; metal ion; copper ion; cytokine;
KW   ceruloplasmin; anticancer; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200117522-A1.
XX
PD   15-MAR-2001.
XX
PF   15-NOV-1999;   99WO-US27193.
XX
PR   08-SEP-1999;   99US-0392122.
XX
PA   (CHAR-) CHARLOTTE-MECKLENBURG HOSPITAL AUTHORITY.
XX
PI   Kennedy TP;
XX
DR   WPI; 2001-281426/29.
XX
PT   Treating cancer, e.g. melanoma, lung cancer, breast cancer or prostatic
PT   carcinoma, comprises administration of a thiuram disulfide optionally
PT   in combination with a heavy metal ion, ceruloplasmin or a cytokine e.g.
PT   interferon-alpha -
XX
PS   Disclosure; Page 24; 60pp; English.
XX
CC   The present invention describes a method for treating established cancer
CC   in a mammal. The method comprises administering a thiuram disulfide (I).
CC   (I) has anticancer and cytostatic activities. (I) induces apoptosis and
CC   G2 cell-cycle arrest, by reducing expression of cyclin A (by preventing
CC   binding of transcription factors to DNA regulatory elements involved in
CC   control of cyclin A expression). The method can be used to treat cancers,
CC   e.g. melanoma, non-small cell lung cancer, small cell lung cancer, renal
CC   cancer, colorectal cancer, breast cancer, pancreatic cancer, gastric
CC   cancer, bladder cancer, ovarian cancer, uterine cancer, lymphoma and
CC   prostate cancer, especially melanoma, lung cancer, breast cancer and
CC   prostate carcinoma. The tumour-inhibiting effect of (I) is dependent on
CC   heavy metal ions, so administering (I) together with such ions (or with
CC   their intracellular carriers, e.g. ceruloplasmin or with serum
CC   ceruloplasmin stimulants, e.g. interferon-alpha) will increase the
CC   antiproliferative/antineoplastic affect. (I) also potentiates the
CC   effect of standard anticancer agents. (I) is already known for treating
CC   alcohol abuse (inhibitor of aldehyde dehydrogenase) and is relatively
CC   nontoxic and safe. The present sequence represents a cyclic-AMP
CC   responsive element CRE consensus oligonucleotide for use in an
CC   electrophoretic mobility shift assay (EMSA), which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match            100.0%;  Score 20;  DB 22;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 13
AAF87957/c
ID   AAF87957 standard; DNA; 27 BP.
XX
AC   AAF87957;
XX
DT   20-JUL-2001  (first entry)
XX
DE   Cyclic-AMP responsive element CRE consensus oligo for EMSA #2.
XX
```

```
KW   Cyclic-AMP responsive element; electrophoretic mobility shift assay;
KW   EMSA; CRE; NF-kappaB; cancer; tetraethyl thiuram disulphide;
KW   dithiocarbamate; tumour; metal ion; copper ion; cytokine;
KW   ceruloplasmin; anticancer; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200117522-A1.
XX
PD   15-MAR-2001.
XX
PF   15-NOV-1999;   99WO-US27193.
XX
PR   08-SEP-1999;   99US-0392122.
XX
PA   (CHAR-) CHARLOTTE-MECKLENBURG HOSPITAL AUTHORITY.
XX
PI   Kennedy TP;
XX
DR   WPI; 2001-281426/29.
XX
PT   Treating cancer, e.g. melanoma, lung cancer, breast cancer or prostatic
PT   carcinoma, comprises administration of a thiuram disulfide optionally
PT   in combination with a heavy metal ion, ceruloplasmin or a cytokine e.g.
PT   interferon-alpha -
XX
PS   Disclosure; Page 24; 60pp; English.
XX
CC   The present invention describes a method for treating established cancer
CC   in a mammal. The method comprises administering a thiuram disulfide (I).
CC   (I) has anticancer and cytostatic activities. (I) induces apoptosis and
CC   G2 cell-cycle arrest, by reducing expression of cyclin A (by preventing
CC   binding of transcription factors to DNA regulatory elements involved in
CC   control of cyclin A expression). The method can be used to treat cancers,
CC   e.g. melanoma, non-small cell lung cancer, small cell lung cancer, renal
CC   cancer, colorectal cancer, breast cancer, pancreatic cancer, gastric
CC   cancer, bladder cancer, ovarian cancer, uterine cancer, lymphoma and
CC   prostate cancer, especially melanoma, lung cancer, breast cancer and
CC   prostate carcinoma. The tumour-inhibiting effect of (I) is dependent on
CC   heavy metal ions, so administering (I) together with such ions (or with
CC   their intracellular carriers, e.g. ceruloplasmin or with serum
CC   ceruloplasmin stimulants, e.g. interferon-alpha) will increase the
CC   antiproliferative/antineoplastic affect. (I) also potentiates the
CC   effect of standard anticancer agents. (I) is already known for treating
CC   alcohol abuse (inhibitor of aldehyde dehydrogenase) and is relatively
CC   nontoxic and safe. The present sequence represents a cyclic-AMP
CC   responsive element CRE consensus oligonucleotide for use in an
CC   electrophoretic mobility shift assay (EMSA), which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 27 BP; 5 A; 9 C; 5 G; 8 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGAG 20
           ||||||||||||||||||||
Db      24 GATTGCCTGACGTCAGAGAG 5


RESULT 14
AAF76267
ID   AAF76267 standard; DNA; 27 BP.
XX
AC   AAF76267;
XX
DT   05-JUN-2001  (first entry)
XX
DE   cAMP response element (CRE) competitor EMSA probe.
XX
KW   NF-kappa-B; nuclear factor-kappa-B; cAMP response element; CRE;
KW   nuclear translocation inhibition; heparin; internalisation;
KW   NF-kappa-B dependent gene expression inhibition; cytokine;
KW   tumour necrosis factor; TNF; interleukin; IL-1; IL-2; IL-6; IL-8;
KW   interferon-beta; interferon-gamma; tissue factor-1; complement;
KW   inducible nitric oxide synthase; diabetic vascular disease;
KW   heart failure; asthma; sepsis; ischaemic-reperfusion injury;
KW   electrophoretic mobility shift assay; competitor EMSA probe; ds.
XX
OS   Unidentified.
XX
PN   WO200119376-A2.
XX
PD   22-MAR-2001.
XX
PF   12-SEP-2000; 2000WO-US24910.
XX
PR   13-SEP-1999;   99US-0395081.
XX
PA   (CHAR-) CHARLOTTE-MECKLENBURG HOSPITAL AUTHORITY.
XX
PI   Kennedy TP;
XX
DR   WPI; 2001-244698/25.
XX
PT   Inhibiting NF-kappa-B activity, useful for treating e.g. diabetic
PT   vascular disease, heart failure, asthma and sepsis, comprises
PT   administering heparin to cells in patient to inhibit translocation of
PT   NF-kappa-B from cytoplasm to nucleus -
XX
PS   Examples; Page 22; 68pp; English.
XX
CC   The invention relates to a method of inhibiting nuclear factor-kappa-B
CC   (NF-kappa-B) activity in a patient, comprising the administration of
CC   heparin to the cells in the patient, such that the heparin is
CC   internalised into the cytoplasm of cells in the patient. The invention
CC   is based on the discovery that heparin is able to block the
CC   translocation of NF-kappa-B from the cytoplasm to the nucleus. This in
CC   turn inhibits NF-kappa-B dependent gene expression. Such NF-kappa-B
CC   dependent genes include genes encoding cytokines such as tumour necrosis
CC   factor (TNF), IL-1 (interleukin-1), IL-2, IL-6, IL-8, interferon-beta,
CC   interferon-gamma, tissue factor-1, complement and inducible nitric
CC   oxide synthase. The method of the invention is used for treating or
CC   preventing diabetic vascular disease, heart failure, asthma, sepsis and
CC   ischaemic-reperfusion injury. Heparin may be administered in combination
CC   with other active agents that treat or prevent another disease or
CC   symptom in the patient, e.g., antiviral agents, antibiotics, antifungal
CC   agents and antiinflammatory agents. The method of the invention offers
CC   significant advantages over prior art treatments for the above
CC   conditions. Heparin is relatively non-toxic and safe, and should not
CC   produce the side effects such as hypertension, glucose intolerance
CC   and bone demineralisation that are encountered with the use of
CC   glucocorticoids for blocking the NF-kappa-B nuclear translocation.
CC   Additionally, heparin is readily available and easily used. Sequences
CC   AAF76266-AAF76267 represents EMSA (electrophoretic mobility shift assay)
CC   probes used to measure the effect of heparin on NF-kappa-B nuclear
CC   translocation. EMSA probe AAF76266 comprises a consensus NF-kappa-B
CC   response element, and EMSA competitor probe AAF76267 comprises a
CC   cAMP response element (CRE).
XX
SQ   Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

  Query Match             100.0%;  Score 20;  DB 22;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GATTGCCTGACGTCAGAGAG 20
           ||||||||||||||||||||
Db       4 GATTGCCTGACGTCAGAGAG 23


RESULT 15
ABA92274
ID   ABA92274 standard; DNA; 27 BP.
XX
```

AC ABA92274;
XX
DT 10-JUN-2002 (first entry)
XX
DE CRE binding site oligonucleotide, used in EMSA.
XX
KW CRE; electrophoretic mobility shift assay; EMSA; ds.
XX
OS Homo sapiens.
XX
PN WO200215912-A1.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26527.
XX
PR 25-AUG-2000; 2000US-228201P.
PR 26-OCT-2000; 2000US-243295P.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Ratan RR, Chatterjee S;
XX
DR WPI; 2002-242023/29.
XX
PT Diagnosing and treating diseases associated with oxidative stress, DNA
PT damage or growth factor depletion, e.g. Alzheimer's and Parkinson's, by
PT administering e.g. mithramycin, chromomycin, daunomycin, olivomycin and
PT WP631 -
XX
PS Example 1; Page 23; 69pp; English.
XX
CC The present sequence is that of a CRE binding site oligonucleotide,
CC which was radiolabelled and used in an electrophoretic mobility shift
CC assay (EMSA) to parallel an EMSA performed with Sp-1 oligonucleotides
CC (see ABA92271-72). The EMSAs were used to determine the effect of
CC oxidative stress on Sp-1 DNA binding, and the effects of candidate
CC compounds on Sp-1 protein levels. SP-1 DNA binding activity in
CC cortical neurons was shown to be low, but was dramatically enhanced
CC by oxidative stress. The invention provides methods for detecting
CC and treating diseases associated with oxidative stress, DNA damage
CC or growth factor depletion, and identifying agents for their
CC treatment. A compound is deemed to be an inhibitor of oxidative
CC stress, DNA damage, growth factor depletion or cell death if it
CC reduces the protein level of an Sp family member or if it decreases
CC the binding of an Sp family member to DNA. A method for preventing
CC or treating a disease or disorder of the nervous system, the ageing
CC process or associated with apoptosis involves administering a
CC compound that inhibits the induction of an Sp family member or the
CC binding of an Sp family member to DNA, e.g. mithramycin,
CC chromomycin, daunomycin, olivomycin or WP631. Diseases and
CC disorders that can be treated include Alzheimer's disease,
CC Creutzfeldt-Jacob disease, kuru, Huntington's disease, aneurysm,
CC stroke associated with an increase in blood pressure, spinal cord
CC disease, spinal cord injury, brain injury, multiple system atrophy,
CC amylotrophic lateral sclerosis, progressive supranuclear palsy,
CC neurodegeneration associated with the ageing process, mitochondrial
CC disease, HIV infection, herpes infection and multiple sclerosis
CC (all claimed).
XX
SQ Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GATTGCCTGACGTCAGAGAG 20
           ||||||||||||||||||||
Db       4 GATTGCCTGACGTCAGAGAG 23
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Job time : 107.319 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:05:40 ; Search time 22.2464 Seconds
(without alignments)
275.709 Million cell updates/sec

Title: US-09-355-254F-17
Perfect score: 20
Sequence: 1 tatgcatattcctgtaagtg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	80.0	19	1	US-08-410-780A-75	Sequence 75, Appl
	2	16	80.0	19	1	US-08-411-020-40	Sequence 40, Appl
	3	16	80.0	19	5	PCT-US95-04511-75	Sequence 75, Appl
	4	15	75.0	17	1	US-08-369-796-21	Sequence 21, Appl
	5	15	75.0	17	2	US-08-852-091-21	Sequence 21, Appl
	6	15	75.0	17	5	PCT-US95-17025-21	Sequence 21, Appl
c	7	15	75.0	19	1	US-08-410-780A-76	Sequence 76, Appl
c	8	15	75.0	19	1	US-08-411-020-41	Sequence 41, Appl
c	9	15	75.0	19	5	PCT-US95-04511-76	Sequence 76, Appl
c	10	14.8	74.0	47	1	US-08-171-389-37	Sequence 37, Appl
c	11	14.8	74.0	47	1	US-08-123-936-37	Sequence 37, Appl
c	12	14.8	74.0	47	2	US-08-475-228A-37	Sequence 37, Appl
c	13	14.8	74.0	47	3	US-08-482-080A-37	Sequence 37, Appl
c	14	14.8	74.0	47	4	US-09-354-947-37	Sequence 37, Appl
c	15	14.8	74.0	47	5	PCT-US93-12388-37	Sequence 436, App
c	16	14.8	74.0	50	1	US-08-171-389-436	Sequence 437, App
c	17	14.8	74.0	50	1	US-08-171-389-437	Sequence 436, App
c	18	14.8	74.0	50	1	US-08-123-936-436	Sequence 437, App
c	19	14.8	74.0	50	1	US-08-123-936-437	Sequence 436, App
c	20	14.8	74.0	50	2	US-08-475-228A-436	Sequence 437, App
c	21	14.8	74.0	50	2	US-08-475-228A-437	Sequence 436, App
c	22	14.8	74.0	50	3	US-08-482-080A-436	Sequence 437, App
c	23	14.8	74.0	50	3	US-08-482-080A-437	Sequence 436, App
c	24	14.8	74.0	50	4	US-09-354-947-436	Sequence 437, App
c	25	14.8	74.0	50	4	US-09-354-947-437	Sequence 436, App
c	26	14.8	74.0	50	5	PCT-US93-12388-436	Sequence 437, App
c	27	14.8	74.0	50	5	PCT-US93-12388-437	
	28	14.4	72.0	19	1	US-08-410-780A-23	Sequence 23, Appl
	29	14.4	72.0	19	1	US-08-410-780A-25	Sequence 25, Appl
	30	14.4	72.0	19	1	US-08-410-780A-33	Sequence 33, Appl
	31	14.4	72.0	19	1	US-08-410-780A-49	Sequence 49, Appl
	32	14.4	72.0	19	1	US-08-410-780A-51	Sequence 51, Appl
	33	14.4	72.0	19	1	US-08-410-780A-55	Sequence 55, Appl
	34	14.4	72.0	19	1	US-08-411-020-42	Sequence 42, Appl
	35	14.4	72.0	19	5	PCT-US95-04511-23	Sequence 23, Appl
	36	14.4	72.0	19	5	PCT-US95-04511-25	Sequence 25, Appl
	37	14.4	72.0	19	5	PCT-US95-04511-33	Sequence 33, Appl
	38	14.4	72.0	19	5	PCT-US95-04511-49	Sequence 49, Appl
	39	14.4	72.0	19	5	PCT-US95-04511-51	Sequence 51, Appl
	40	14.4	72.0	19	5	PCT-US95-04511-55	Sequence 55, Appl
	41	14	70.0	20	4	US-09-489-868A-31	Sequence 31, Appl
c	42	13.4	67.0	19	1	US-08-410-780A-24	Sequence 24, Appl
c	43	13.4	67.0	19	1	US-08-410-780A-26	Sequence 26, Appl
c	44	13.4	67.0	19	1	US-08-410-780A-34	Sequence 34, Appl
c	45	13.4	67.0	19	1	US-08-410-780A-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-410-780A-75
; Sequence 75, Application US/08410780A
; Patent No. 5707803
; GENERAL INFORMATION:
; APPLICANT: LAMB, I. PETER
; APPLICANT: SEIDEL, H. MARTI
; TITLE OF INVENTION: DNA REGULATORY ELEMENTS RESPONSIVE TO
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,780A
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,934
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0017A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
;
US-08-410-780A-75

Query Match 80.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       5 CATATTCCTGTAAGTG 20
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Db       4 CATATTCCTGTAAGTG 19


RESULT 2
US-08-411-020-40
; Sequence 40, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-40

  Query Match             80.0%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 CATATTCCTGTAAGTG 20
           ||||||||||||||||
Db       4 CATATTCCTGTAAGTG 19


RESULT 3
PCT-US95-04511-75
; Sequence 75, Application PC/TUS9504511
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  DNA REGULATORY ELEMENTS RESPONSIVE TO
;    TITLE OF INVENTION:  CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  76
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04511
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/228,934
;      FILING DATE:  14-APR-1994
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
PCT-US95-04511-75

  Query Match             80.0%;  Score 16;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 CATATTCCTGTAAGTG 20
           ||||||||||||||||
Db       4 CATATTCCTGTAAGTG 19


RESULT 4
US-08-369-796-21
; Sequence 21, Application US/08369796
; Patent No. 5716622
;  GENERAL INFORMATION:
;    APPLICANT:  James E. Darnell, Jr.
;    APPLICANT:  Zilong Wen
;    APPLICANT:  Curt M. Horvath
;    APPLICANT:  Zhong Zhong
;    TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;    TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/369,796
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA synthetic probe
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-369-796-21
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```
  Query Match             75.0%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 ATATTCCTGTAAGTG 20
          |||||||||||||||
Db      1 ATATTCCTGTAAGTG 15


RESULT 5
US-08-852-091-21
; Sequence 21, Application US/08852091
; Patent No. 5883228
;  GENERAL INFORMATION:
;    APPLICANT:  James E. Darnell, Jr.
;    APPLICANT:  Zilong Wen
;    APPLICANT:  Curt M. Horvath
;    APPLICANT:  Zhong Zhong
;    TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;    TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/852,091
;      FILING DATE:  06-MAY-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/369,796
;      FILING DATE:  06-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA synthetic probe
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-852-091-21

  Query Match             75.0%;  Score 15;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 ATATTCCTGTAAGTG 20
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Db      1 ATATTCCTGTAAGTG 15


RESULT 6
PCT-US95-17025-21
; Sequence 21, Application PC/TUS9517025
;  GENERAL INFORMATION:
;    APPLICANT:  James E. Darnell, Jr.
;    APPLICANT:  Zilong Wen
;    APPLICANT:  Curt M. Horvath
;    APPLICANT:  Zhong Zhong
;    TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;    TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/17025
;      FILING DATE:  28-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/369,796
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA synthetic probe
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-17025-21

  Query Match             75.0%;  Score 15;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 ATATTCCTGTAAGTG 20
          |||||||||||||||
Db      1 ATATTCCTGTAAGTG 15


RESULT 7
US-08-410-780A-76/c
; Sequence 76, Application US/08410780A
; Patent No. 5707803
;  GENERAL INFORMATION:
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  SEIDEL, H. MARTI
;    TITLE OF INVENTION:  DNA REGULATORY ELEMENTS RESPONSIVE TO
;    TITLE OF INVENTION:  CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LIGAND PHARMACEUTICALS INCORPORATED
;      STREET:  9393 TOWNE CENTRE DRIVE
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/410,780A
;       FILING DATE:  27-MAR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/228,934
;       FILING DATE:  14-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  JURGENSEN, THOMAS E
;       REGISTRATION NUMBER:  34,195
;       REFERENCE/DOCKET NUMBER:  016-0017A.US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 550-7675
;       TELEFAX:  (619) 535-3906
;   INFORMATION FOR SEQ ID NO:  76:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;       DESCRIPTION:  SYNTHETIC DNA"
US-08-410-780A-76

  Query Match             75.0%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ATATTCCTGTAAGTG 20
           |||||||||||||||
Db      19 ATATTCCTGTAAGTG 5


RESULT 8
US-08-411-020-41/c
; Sequence 41, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-41

  Query Match             75.0%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ATATTCCTGTAAGTG 20
           |||||||||||||||
Db      19 ATATTCCTGTAAGTG 5


RESULT 9
PCT-US95-04511-76/c
; Sequence 76, Application PC/TUS9504511
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  DNA REGULATORY ELEMENTS RESPONSIVE TO
;    TITLE OF INVENTION:  CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUÈNCES:  76
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04511
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/228,934
;      FILING DATE:  14-APR-1994
;  INFORMATION FOR SEQ ID NO:  76:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
PCT-US95-04511-76

  Query Match             75.0%;  Score 15;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ATATTCCTGTAAGTG 20
           |||||||||||||||
Db      19 ATATTCCTGTAAGTG 5


RESULT 10
US-08-171-389-37/c
; Sequence 37, Application US/08171389
; Patent No. 5578444
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
```

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;       ADDRESSEE:  Genelabs Technologies, Inc.
;       STREET:  505 Penobscot Drive
;       CITY:  Redwood City
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94063
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/171,389
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/123,936
;       FILING DATE:  17-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/996,783
;       FILING DATE:  23-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/723,618
;       FILING DATE:  27-JUN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/081,070
;       FILING DATE:  22-JUN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fabian, Gary R.
;       REGISTRATION NUMBER:  33,875
;       REFERENCE/DOCKET NUMBER:  4600-0175/G19P3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 324-0880
;       TELEFAX:  (415) 324-0960
;   INFORMATION FOR SEQ ID NO:  37:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  47 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  Human alpha-amylase gene
US-08-171-389-37

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 67;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      28 TATTTATATTCCTGTAAG 11


RESULT 11
US-08-123-936-37/c
; Sequence 37, Application US/08123936
; Patent No. 5726014
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    TITLE OF INVENTION:  Screening Assay for the Detection of
;    TITLE OF INVENTION:  DNA-Binding Molecules
;    NUMBER OF SEQUENCES:  640
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/123,936
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0075.32/G19P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human alpha-amylase gene
US-08-123-936-37

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 67;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      28 TATTTATATTCCTGTAAG 11


RESULT 12
US-08-475-228A-37/c
; Sequence 37, Application US/08475228A
; Patent No. 5869241
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,228A
;      FILING DATE:  06-JUN-1995
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stratford, Carol A.
;      REGISTRATION NUMBER:  34,444
;      REFERENCE/DOCKET NUMBER:  4600-0175.21/G19P3D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human alpha-amylase gene
US-08-475-228A-37

  Query Match             74.0%;  Score 14.8;  DB 2;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 67;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


RESULT 13
US-08-482-080A-37/c
; Sequence 37, Application US/08482080A
; Patent No. 6010849
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,080A
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/171,389
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brady, John F.
;      REGISTRATION NUMBER:  39,118
;      REFERENCE/DOCKET NUMBER:  4600-0175.20/G19P3D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human alpha-amylase gene
US-08-482-080A-37

  Query Match             74.0%;  Score 14.8;  DB 3;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 67;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


RESULT 14
US-09-354-947-37/c
; Sequence 37, Application US/09354947
; Patent No. 6384208
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Cynthia A.
;    APPLICANT:  Cantor, Charles R.
;    APPLICANT:  Andrews, Beth M.
;    APPLICANT:  Turin, Lisa M.
;    APPLICANT:  Fry, Kirk E.
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  664
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/354,947
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/482,080
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/171,389
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/723,618
;      FILING DATE:  27-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,070
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brady, John F.
;      REGISTRATION NUMBER:  39,118
;      REFERENCE/DOCKET NUMBER:  4600-0175.20/G19P3D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 324-0880
;      TELEFAX:  (650) 324-0960
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human alpha-amylase gene
US-09-354-947-37

  Query Match             74.0%;  Score 14.8;  DB 4;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 67;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


RESULT 15
PCT-US93-12388-37/c
; Sequence 37, Application PC/TUS9312388
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Sequence-Directed DNA Binding
;    TITLE OF INVENTION:  Molecules, Compositions and Methods
;    NUMBER OF SEQUENCES:  641
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genelabs Technologies, Inc.
;      STREET:  505 Penobscot Drive
;      CITY:  Redwood City
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94063
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12388
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,936
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/996,783
;      FILING DATE:  23-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  4600-0175.41/G19PCT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Human alpha-amylase gene
PCT-US93-12388-37

  Query Match             74.0%;  Score 14.8;  DB 5;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 67;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11


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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Title: US-09-355-254F-17
Perfect score: 20
Sequence: 1 tatgcatattcctgtaagtg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	19	AAV46009	Immune adjuvant ST
	2	20	100.0	20	24	AAL39193	Murine Toll-like r
	3	19	95.0	24	24	ABN80818	Human STAT-1 inhib
	4	16	80.0	19	17	AAT41604	Oligonucleotide co
	5	15	75.0	17	17	AAT31283	STAT probe Ly6E.
c	6	14.8	74.0	47	15	AAQ69287	Human alpha-amylas
c	7	14.8	74.0	47	18	AAT63749	Human alpha amylas
c	8	14.8	74.0	47	20	AAX17037	Test sequence from
c	9	14.8	74.0	47	24	ABK82528	DNA binding molecu
c	10	14.8	74.0	50	15	AAQ69686	Human pancreatic a
c	11	14.8	74.0	50	15	AAQ69687	Human pancreatic a
c	12	14.8	74.0	50	18	AAT64148	Human pancreatic a
c	13	14.8	74.0	50	18	AAT64149	Human pancreatic a
c	14	14.8	74.0	50	20	AAX17436	Test sequence from
c	15	14.8	74.0	50	20	AAX17437	Test sequence from
c	16	14.8	74.0	50	24	ABK82927	DNA binding molecu
c	17	14.8	74.0	50	24	ABK82928	DNA binding molecu
	18	14.4	72.0	19	17	AAT41605	Oligonucleotide co
	19	14	70.0	20	22	AAD11323	Human cot oncogene
c	20	14	70.0	27	15	AAT14907	Primer 2 for pMAL-
c	21	14	70.0	27	15	AAQ55426	CZP-3 Gene primer.
	22	13.8	69.0	22	21	AAC71335	Single nucleotide
	23	13.6	68.0	50	19	AAV66651	Anti-human Fas hum
	24	13.6	68.0	50	21	AAA78342	Humanised anti-Fas
c	25	13.4	67.0	21	20	AAX33318	PEBP2 alpha A gene
c	26	13.4	67.0	24	24	ABQ01109	Oligonucleotide ad
c	27	13.4	67.0	24	24	ABQ06151	Oligonucleotide ad
	28	13.4	67.0	24	24	ABQ06192	Oligonucleotide ad
c	29	13.4	67.0	25	22	AAH39126	SNP specific lower
	30	13.4	67.0	51	22	AAI79532	Human silent SNP c
	31	13.4	67.0	60	14	AAQ51030	5' fragment of the
	32	13.4	67.0	60	24	ABN39544	Human spliced tran
	33	13.2	66.0	21	22	AAF87028	Sequencing primer
c	34	13.2	66.0	31	20	AAX38743	Human genomic DNA
	35	13.2	66.0	60	24	ABN36070	Human spliced tran
	36	13.2	66.0	65	24	ABN29969	Rat spliced transc
	37	13.2	66.0	99	21	AAZ42637	Human 5' EST isola
	38	13	65.0	13	16	AAT02747	Ly6 GAS regulatory
c	39	13	65.0	47	21	AAZ66670	Human map-related
	40	13	65.0	65	24	ABN52711	Mouse spliced tran
	41	12.8	64.0	23	20	AAX52734	Human genome biall
c	42	12.8	64.0	36	13	AAQ31180	PCR primer #2 for
	43	12.8	64.0	41	24	ABK48179	Citrate synthase 1
	44	12.8	64.0	47	20	AAX52584	Human genome biall
	45	12.8	64.0	47	20	AAX52534	Human genome biall

ALIGNMENTS

RESULT 1
AAV46009
ID AAV46009 standard; DNA; 20 BP.
XX
AC AAV46009;
XX
DT 16-OCT-1998 (first entry)
XX
DE Immune adjuvant STAT1.
XX
KW Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;
KW modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;
KW Ig class; autoimmune response; T-cell; B-cell; tumour; ss.
XX
OS Class Bacteria.
XX
PN EP855184-A1.
XX
PD 29-JUL-1998.
XX
PF 23-JAN-1997; 97EP-0101019.
XX
PR 23-JAN-1997; 97EP-0101019.
XX
PA (HEEG/) HEEG K.
PA (LIPF/) LIPFORD G B.
PA (WAGN/) WAGNER H.
XX
PI Heeg K, Lipford GB, Wagner H;
XX
DR WPI; 1998-389630/34.
XX

PT Antigenic composition comprises polynucleotide fragment and antigen
PT - used as vaccine to treat or prevent e.g. cancer or pathogen
PT infections and to modulate immune response e.g. tolerance break and
PT regulation of TH1/TH2 cells
XX
PS Example 5; Page 9; 28pp; English.
XX
CC AAV45993-V46019 are fragments of bacterial polynucleotides which are
CC used as immune adjuvants for inclusion into vaccines to treat cancer and
CC for prophylaxis and/or treatment of conditions caused by pathogenic
CC micro-organisms. The polynucleotide is used for modulation of an immune
CC response and the modulation is selected from the group break of
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig
CC classes, treatment of autoimmune responses and induction of tolerances.
CC DNA oligomers are used to enhance the reactivity of immune cells to
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination
CC against tumour-defined antigens and immunostimulatory substances in an
CC immune response against tumours and to suppress immune reactions of the
CC innate and acquired immune system. The composition is inexpensive and
CC stable and does not cause lethal shock, which happens with prior art
CC bacterial sequences.
XX
SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGCATATTCCTGTAAGTG 20
||||||||||||||||||||
Db 1 TATGCATATTCCTGTAAGTG 20

RESULT 2
AAL39193
ID AAL39193 standard; DNA; 20 BP.
XX
AC AAL39193;
XX
DT 05-SEP-2002 (first entry)
XX
DE Murine Toll-like receptor related CpG DNA SEQ ID No 68.
XX
KW Murine Toll-like receptor; TLR9; TLR7; TLR8; ISNA; ds.
XX
OS Unidentified.
XX
PN WO200222809-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US29229.
XX
PR 15-SEP-2000; 2000US-233035P.
PR 23-JAN-2001; 2001US-263657P.
PR 17-MAY-2001; 2001US-291726P.
PR 22-JUN-2001; 2001US-300210P.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Bauer S, Lipford G, Wagner H;
XX
DR WPI; 2002-393964/42.
XX
PT New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides,
PT useful for identifying species specificity of immunostimulatory nucleic
PT acid and identifying immunostimulatory nucleic acids -
XX
PS Disclosure; Page 76; 195pp; English.
XX
CC The invention relates to isolated murine Toll-like receptors (TLR)9,
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The
CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC TLR7, TLR8 and TLR9 polypeptides are also useful for comparing TLR9
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide
CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention.
XX
SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGCATATTCCTGTAAGTG 20
||||||||||||||||||||
Db 1 TATGCATATTCCTGTAAGTG 20

RESULT 3
ABN80818
ID ABN80818 standard; DNA; 24 BP.
XX
AC ABN80818;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human STAT-1 inhibitor oligonucleotide SEQ ID NO 36.
XX
KW Human; IRF-1; transcription factor; interferon regulatory factor;
KW antisense; gene therapy; cardiovascular; transplant rejection;
KW immunological hypersensitivity; asthma; inflammatory disease; psoriasis;
KW Crohn's disease; autoimmune disease; diabetes mellitus;
KW multiple sclerosis; rheumatoid arthritis; Th1 response; Th2 response;
KW vasotropic; immunosuppressive; antiasthmatic; dermatological;
KW antiallergic; antiulcer; antiinflammatory; antipsoriatic; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200229044-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-DE03835.
XX
PR 06-OCT-2000; 2000DE-1049549.
PR 29-NOV-2000; 2000DE-1059144.
XX
PA (HECK/) HECKER M.
PA (WAGN/) WAGNER A H.
XX
PI Hecker M, Wagner AH;
XX
DR WPI; 2002-383335/41.
XX
PT Inhibitor of the transcription factor IFR-1, useful for treating e.g.
PT transplant rejection and autoimmune disease, reduces expression of CD40
PT -
XX
PS Example 3; Page 19; 45pp; German.
XX

```
CC   The invention relates to an inhibitor (I) of the expression and/or
CC   activity of the transcription factor (IRF-1; interferon regulatory
CC   factor) as a therapeutic agent, especially an oligonucleotide inhibitor
CC   (ABN80783-ABN80804) or antisense oligonucleotide (ABN80805-ABN80808) used
CC   in antisense gene therapy. (I) are used to prevent or treat
CC   cardiovascular complications such as restenosis after angioplasty or
CC   stenosis of venous by-passes, chronic or acute transplant rejection and
CC   graft versus host disease, immunological hypersensitivity, e.g. bronchial
CC   asthma or atopic dermatitis, inflammatory diseases such as ulcerative
CC   colitis, psoriasis and Crohn's disease and autoimmune diseases such as
CC   diabetes mellitus, multiple sclerosis, collagenosis (e.g. systemic lupus
CC   erythematosus), rheumatoid arthritis and vasculitis. (I) simultaneously
CC   weaken both Th1 and Th2 responses. The present sequence is that of an
CC   oligonucleotide, useful to the invention.
XX
SQ   Sequence 24 BP; 6 A; 4 C; 4 G; 10 T; 0 other;

  Query Match             95.0%;  Score 19;  DB 24;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAGT 19
           |||||||||||||||||||
Db       6 TATGCATATTCCTGTAAGT 24


RESULT 4
AAT41604
ID   AAT41604 standard; DNA; 19 BP.
XX
AC   AAT41604;
XX
DT   04-JUN-1997  (first entry)
XX
DE   Oligonucleotide containing core DNA regulatory element.
XX
KW   Regulatory element; STAT; protein; cytokine; responsive;
KW   host cell; transfection; agonist; antagonist; mediated; STAT5;
KW   transcription; modulation; signalling pathway; STAT6;
KW   oligonucleotide; electrophoretic mobility shift assay; EMSA; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    5..19
FT                   /*tag= a
FT                   /note= "core DNA regulatory element"
XX
PN   WO9630515-A1.
XX
PD   03-OCT-1996.
XX
PF   25-MAR-1996;   96WO-US04012.
XX
PR   27-MAR-1995;   95US-0411020.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM,  Tian Chan S;
XX
DR   WPI; 1996-455362/45.
XX
PT   DNA construct for screening modulators of cytokine-mediated
PT   transcription  - contg. regulatory element and a cytokine-sensitive
PT   promoter operably linked to a heterologous gene
XX
PS   Example 1; Page 25; 72pp; English.
XX
CC   A novel DNA construct comprises the present oligonucleotide (ON),
CC   which contains a core a regulatory element, operably linked to a
CC   promoter, which is operably linked to a heterologous gene
CC   (preferably a marker gene). The gene is under the transcriptional
CC   control of the promoter and the ON sequence when the ON is bound by
CC   a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,
CC   erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,
CC   IL-13 or IL-15. Cytokine responsive host cells transfected with the
CC   DNA construct can be used to measure the ability of a compound to
CC   act as an agonist or antagonist of cytokine mediated gene
CC   transcription. In particular, they can be used to screen for
CC   cytokine modulators involved in the STAT5 and/or STAT6 protein
CC   signalling pathway.
CC   Following an electrophoretic mobility shift assay the DNA construct
CC   was found to bind IL-4 weakly and IL-13 not determined.
XX
SQ   Sequence 19 BP; 5 A; 3 C; 4 G; 7 T; 0 other;

  Query Match             80.0%;  Score 16;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 CATATTCCTGTAAGTG 20
           ||||||||||||||||
Db       4 CATATTCCTGTAAGTG 19


RESULT 5
AAT31283
ID   AAT31283 standard; DNA; 17 BP.
XX
AC   AAT31283;
XX
DT   24-OCT-1996  (first entry)
XX
DE   STAT probe Ly6E.
XX
KW   STAT; signal transducer and activator of transcription;
KW   DNA binding protein; ligand; receptor; oncogenesis; inflammation;
KW   autoimmune disease; antagonist; gene therapy; probe; ds.
XX
OS   Synthetic.
XX
PN   WO9620954-A2.
XX
PD   11-JUL-1996.
XX
PF   28-DEC-1995;   95WO-US17025.
XX
PR   06-JAN-1995;   95US-0369796.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Darnell JE,  Horvath CM,  Wen Z,  Zhong Z;
XX
DR   WPI; 1996-333941/33.
XX
PT   New STAT protein DNA-binding domain peptide(s) - useful for
PT   diagnosing, preventing or treating cellular dysfunction, e.g.
PT   oncogenesis, inflammation, parasitic disease or autoimmunity
XX
PS   Example 1; Page 42; 138pp; English.
XX
CC   Synthetic DNA probes (AAT31281-86) were used in electrophoretic
CC   mobility shift assays to determine the functionally active
CC   regions of signal transducer and activator of transcription
CC   (STAT) proteins STAT1 (see also AAW03176) and STAT3 (AAW03174).
CC   Amino acids between approx. 400 and approx. 500 of these
CC   human proteins determined DNA binding site specificity.
CC   Mutations within this region resulted in greatly reduced DNA
CC   binding affinities.
XX
SQ   Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 other;

  Query Match             75.0%;  Score 15;  DB 17;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy      6 ATATTCCTGTAAGTG 20
          ||||||||||||||
Db      1 ATATTCCTGTAAGTG 15
```

RESULT 6
AAQ69287/c
ID AAQ69287 standard; DNA; 47 BP.
XX
AC AAQ69287;
XX
DT 21-FEB-1995 (first entry)
XX
DE Human alpha-amylase gene, target region.
XX
KW DNA protein-binding assay; test sequence; screening sequence;
KW promoter; target; TATA box; Herpes Simplex Virus; HSV;
KW origin of replication; UL9; transcription factor; TFIID: ds.
XX
OS Synthetic.
XX
PN WO9414980-A.
XX
PD 07-JUL-1994.
XX
PF 20-DEC-1993; 93WO-US12388.
XX
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1994-234711/28.
XX
PT Sequence-directed DNA-binding molecules - useful in
PT pharmaceuticals and as molecular reagents
XX
PS Claim 28; Page 230; 587pp; English.
XX
CC A DNA protein-binding assay is provided, useful for screening
CC libraries of synthetic or biological cpds. for their ability
CC to bind DNA test sequences. The assay is versatile in that any
CC number of test sequences can be tested by placing the test sequence
CC adjacent to a defined protein-binding screening sequence. Binding
CC of mols. to these test sequences changes the binding characteristics
CC of the protein mol. to its cognate binding sequence. When such a mol.
CC binds the test sequence, the equilibrium of the DNA:protein complexes
CC is disturbed, generating changes in the concentration of free DNA probe.
CC One application of this method is to eucaryotic general transcription
CC factors (e.g. TFIID), where the target region is typically selected
CC from DNA sequences adjacent to the binding site for the eucaryotic
CC transcription factor. Numerous exemplary test sequences are given:
CC the sequences in AAQ69251-731 and AAQ69850 correspond to promoter
CC targets (typically, TATA box-contg. sites) for human genes and the
CC sequences in AAQ69732-849 correspond to promoter targets for viral genes.
CC   The test sequences may also be randomly generated. DNA:protein
CC interaction may be used for screening purposes, e.g. the Herpes Simplex
CC Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and
CC AAQ69891).
XX
SQ Sequence 47 BP; 17 A; 6 C; 10 G; 14 T; 0 other;

```
  Query Match             74.0%;  Score 14.8;  DB 15;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11
```

RESULT 7
AAT63749/c
ID AAT63749 standard; DNA; 47 BP.
XX
AC AAT63749;
XX
DT 13-MAR-1997 (first entry)
XX
DE Human alpha amylase gene TFIID binding site.
XX
KW Duplex DNA; target region; binding characteristic; DNA binding protein;
KW TFIID; transcription factor; binding site; inhibition; enhance;
KW cancer; inherited genetic disorder; ds.
XX
OS Homo sapiens.
XX
PN US5578444-A.
XX
PD 26-NOV-1996.
XX
PF 27-JUN-1991; 91US-0723618.
XX
PR 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1997-020402/02.
XX
PT Altering binding characteristics of DNA binding proteins to duplex
PT DNA - by attaching specific small cpd. to target region close to the
PT protein's binding site, useful in treatment of viral disease, cancer
PT etc
XX
PS Claim 6; Column 117; 264pp; English.
XX
CC The sequences given in AAT63713-4312 represent duplex DNA's which act
CC as target regions in the method of the invention. The method for
CC altering the binding characteristics of a DNA-binding protein to duplex
CC DNA comprises contacting the duplex DNA with a small molecule which
CC binds sequence-specifically to a target region, where, when the small
CC molecule is bound to the target region, it is adjacent to, but not
CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
CC The small molecule is added at a concentration effective to alter the
CC binding of the DNA binding protein, pref. TFIID, to its binding site on
CC the duplex DNA. The binding of the small molecule may inhibit or
CC enhance the binding of the DNA-binding protein to its binding site. The
CC compounds isolated using this method are potentially useful as
CC therapeutic agents for treatment of any disease which involves a
CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
CC The method is suitable for screening large biological or chemical
CC libraries and allows determination of sequence-specific and relative
CC affinities of known DNA-binding agents for different DNA sequences.
CC The design of these duplex DNA's allows a single DNA:protein interaction
CC to be used for screening sequence-specific, or preferential, DNA binding
CC proteins that recognise almost any possible sequence (see also AAT49539-
CC 74).
XX
SQ Sequence 47 BP; 17 A; 6 C; 10 G; 14 T; 0 other;

```
  Query Match             74.0%;  Score 14.8;  DB 18;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TATGCATATTCCTGTAAG 18
          |||  ||||||||||||
Db     28 TATTTATATTCCTGTAAG 11
```

```
RESULT 8
AAX17037/c
ID   AAX17037 standard; DNA; 47 BP.
XX
AC   AAX17037;
XX
DT   06-MAY-1999  (first entry)
XX
DE   Test sequence from human alpha-amylase gene.
XX
KW   Test sequence; DNA-binding molecule; screening sequence; human;
KW   nucleic acid amplification; target; viral; ds.
XX
OS   Homo sapiens.
XX
PN   US5869241-A.
XX
PD   09-FEB-1999.
XX
PF   07-JUN-1995;   95US-0475228.
XX
PR   20-DEC-1993;   93US-0171389.
PR   27-JUN-1991;   91US-0723618.
PR   23-DEC-1992;   92US-0996783.
PR   17-SEP-1993;   93US-0123936.
PR   07-JUN-1995;   95US-0475228.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Andrews BM,  Cantor CR,  Edwards CA,  Fry KE,  Turin LM;
XX
DR   WPI; 1999-152755/13.
XX
PT   Determination of DNA sequence preference of a DNA-binding molecule -
PT   based on inhibition of binding of protein to oligonucleotide
PT   sequence attached to test sequence
XX
PS   Claim 3; Columns 119-120; 270pp; English.
XX
CC   Sequences AAX17001 to AAX17600 represent specifically claimed target
CC   test sequences that are used in the method of the invention of
CC   determining the DNA sequence preference of a DNA-binding molecule. The
CC   method comprises: (i) adding a test molecule and a DNA-binding protein to
CC   a mixture of duplex DNA test oligonucleotides, each of the test
CC   oligonucleotides having a test sequence adjacent to a screening sequence,
CC   where the screening sequence binds to the DNA-binding protein with a
CC   binding affinity that is independent of the DNA sequence of the test
CC   sequence, and where the mixture of duplex DNA test oligonucleotides
CC   includes several test sequences; (ii) incubating the test molecule, the
CC   mixture of duplex DNA test oligonucleotides and the DNA-binding protein
CC   for a time sufficient to permit binding of the test molecule to test
CC   sequences in the duplex DNA; (iii) separating unbound test
CC   oligonucleotides from test oligonucleotides bound to binding protein;
CC   (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
CC   (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
CC   (vii) sequencing the isolated test oligonucleotides. Test sequences
CC   AAX17001-X17481 and AAX17600 correspond to promoter targets for human
CC   genes and test sequences AAX17482-X17599 correspond to promoter targets
CC   for viral genes.
XX
SQ   Sequence 47 BP; 17 A; 6 C; 10 G; 14 T; 0 other;

  Query Match             74.0%;  Score 14.8;  DB 20;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      28 TATTTATATTCCTGTAAG 11


RESULT 9
ABK82528/c
ID   ABK82528 standard; DNA; 47 BP.
XX
AC   ABK82528;
XX
DT   27-AUG-2002  (first entry)
XX
DE   DNA binding molecule screening method test sequence #37.
XX
KW   DNA binding molecule screening; inhibition of transcription;
KW   infection; human immunodeficiency virus; HIV; parasite; cancer;
KW   cardiovascular; respiratory; gastrointestinal; endocrine; metabolic;
KW   rheumatic; immunological; haematological; neurological;
KW   psychiatric; dermatological; ophthalmological; musculo-skeletal;
KW   urogenital disorder; ss.
XX
OS   Synthetic.
XX
PN   US6384208-B1.
XX
PD   07-MAY-2002.
XX
PF   15-JUL-1999;   99US-0354947.
XX
PR   20-DEC-1993;   93US-0171389.
PR   07-JUN-1995;   95US-0482080.
PR   27-JUN-1991;   91US-0723618.
PR   23-DEC-1992;   92US-0996783.
PR   17-SEP-1993;   93US-0123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Edwards CA,  Cantor CR,  Andrews BM,  Turin LM,  Fry KE;
XX
DR   WPI; 2002-442819/47.
XX
PT   Decreasing transcriptional activity of genes for treating infections or
PT   cancer, by administration of an agent that binds to two non-overlapping
PT   regions of the gene  -
XX
PS   Example 15; SEQ ID No 37; 98pp; English.
XX
CC   The invention relates to a method of decreasing transcriptional activity
CC   in a duplex deoxyribonucleic acid (DNA) template (T1) comprising
CC   contacting (T1) with a binding agent comprising at least one small duplex
CC   DNA-binding molecule (T2) coupled to at least one other small duplex-
CC   binding molecule that binds to a non-overlapping region of target
CC   sequence (TS). The method is useful for inhibiting transcription of a
CC   range of disease-related genes for treating infections (by viruses,
CC   including human immunodeficiency virus, bacteria, fungi, protozoa
CC   and parasites), cancer, cardiovascular, respiratory, gastrointestinal,
CC   endocrine/metabolic, rheumatic/immunological, haematological,
CC   neurological, psychiatric, dermatological, ophthalmological,
CC   musculo-skeletal, genetic or urogenital disorders. The method provides
CC   sequence-specific inhibition of transcription of pathological genes
CC   without affecting transcription of cellular genes regulated by the same
CC   transcription factor, and can be applied to regulation of any gene.
CC   ABK82492-ABK83155 represent DNA binding molecule test sequences used in
CC   the method of the invention.
XX
SQ   Sequence 47 BP; 17 A; 6 C; 10 G; 14 T; 0 other;

  Query Match             74.0%;  Score 14.8;  DB 24;  Length 47;
  Best Local Similarity   88.9%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      28 TATTTATATTCCTGTAAG 11


RESULT 10
AAQ69686/c
ID   AAQ69686 standard; DNA; 50 BP.
```

```
XX
AC   AAQ69686;
XX
DT   02-MAR-1995  (first entry)
XX
DE   Human pancreatic alpha-amylase gene, target region.
XX
KW   DNA protein-binding assay; test sequence; screening sequence;
KW   promoter; target; TATA box; Herpes Simplex Virus; HSV;
KW   origin of replication; UL9; transcription factor; TFIID: ds.
XX
OS   Synthetic.
XX
PN   WO9414980-A.
XX
PD   07-JUL-1994.
XX
PF   20-DEC-1993;   93WO-US12388.
XX
PR   23-DEC-1992;   92US-0996783.
PR   17-SEP-1993;   93US-0123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Andrews BM,  Cantor CR,  Edwards CA,  Fry KE,  Turin LM;
XX
DR   WPI; 1994-234711/28.
XX
PT   Sequence-directed DNA-binding molecules - useful in
PT   pharmaceuticals and as molecular reagents
XX
PS   Claim 28; Page 430; 587pp; English.
XX
CC   A DNA protein-binding assay is provided, useful for screening
CC   libraries of synthetic or biological cpds. for their ability
CC   to bind DNA test sequences.  The assay is versatile in that any
CC   number of test sequences can be tested by placing the test sequence
CC   adjacent to a defined protein-binding screening sequence.  Binding
CC   of mols. to these test sequences changes the binding characteristics
CC   of the protein mol. to its cognate binding sequence.  When such a mol.
CC   binds the test sequence, the equilibrium of the DNA:protein complexes
CC   is disturbed, generating changes in the concentration of free DNA probe.
CC   One application of this method is to eucaryotic general transcription
CC   factors (e.g. TFIID), where the target region is typically selected
CC   from DNA sequences adjacent to the binding site for the eucaryotic
CC   transcription factor.  Numerous exemplary test sequences are given:
CC   the sequences in AAQ69251-731 and AAQ69850 correspond to promoter
CC   targets (typically, TATA box-contg. sites) for human genes and the
CC   sequences in AAQ69732-849 correspond to promoter targets for viral genes.
CC    The test sequences may also be randomly generated.  DNA:protein
CC   interaction may be used for screening purposes, e.g. the Herpes Simplex
CC   Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and
CC   AAQ69891).
XX
SQ   Sequence 50 BP; 18 A; 6 C; 10 G; 16 T; 0 other;

  Query Match             74.0%;  Score 14.8;  DB 15;  Length 50;
  Best Local Similarity   88.9%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      32 TATTTATATTCCTGTAAG 15


RESULT 11
AAQ69687/c
ID   AAQ69687 standard; DNA; 50 BP.
XX
AC   AAQ69687;
XX
DT   02-MAR-1995  (first entry)
XX
DE   Human pancreatic alpha-amylase gene, target region.
XX
KW   DNA protein-binding assay; test sequence; screening sequence;
KW   promoter; target; TATA box; Herpes Simplex Virus; HSV;
KW   origin of replication; UL9; transcription factor; TFIID: ds.
XX
OS   Synthetic.
XX
PN   WO9414980-A.
XX
PD   07-JUL-1994.
XX
PF   20-DEC-1993;   93WO-US12388.
XX
PR   23-DEC-1992;   92US-0996783.
PR   17-SEP-1993;   93US-0123936.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Andrews BM,  Cantor CR,  Edwards CA,  Fry KE,  Turin LM;
XX
DR   WPI; 1994-234711/28.
XX
PT   Sequence-directed DNA-binding molecules - useful in
PT   pharmaceuticals and as molecular reagents
XX
PS   Claim 28; Page 430; 587pp; English.
XX
CC   A DNA protein-binding assay is provided, useful for screening
CC   libraries of synthetic or biological cpds. for their ability
CC   to bind DNA test sequences.  The assay is versatile in that any
CC   number of test sequences can be tested by placing the test sequence
CC   adjacent to a defined protein-binding screening sequence.  Binding
CC   of mols. to these test sequences changes the binding characteristics
CC   of the protein mol. to its cognate binding sequence.  When such a mol.
CC   binds the test sequence, the equilibrium of the DNA:protein complexes
CC   is disturbed, generating changes in the concentration of free DNA probe.
CC   One application of this method is to eucaryotic general transcription
CC   factors (e.g. TFIID), where the target region is typically selected
CC   from DNA sequences adjacent to the binding site for the eucaryotic
CC   transcription factor.  Numerous exemplary test sequences are given:
CC   the sequences in AAQ69251-731 and AAQ69850 correspond to promoter
CC   targets (typically, TATA box-contg. sites) for human genes and the
CC   sequences in AAQ69732-849 correspond to promoter targets for viral genes.
CC    The test sequences may also be randomly generated.  DNA:protein
CC   interaction may be used for screening purposes, e.g. the Herpes Simplex
CC   Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and
CC   AAQ69891).
XX
SQ   Sequence 50 BP; 18 A; 6 C; 10 G; 16 T; 0 other;

  Query Match             74.0%;  Score 14.8;  DB 15;  Length 50;
  Best Local Similarity   88.9%;  Pred. No. 5.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TATGCATATTCCTGTAAG 18
           |||  ||||||||||||
Db      32 TATTTATATTCCTGTAAG 15


RESULT 12
AAT64148/c
ID   AAT64148 standard; DNA; 50 BP.
XX
AC   AAT64148;
XX
DT   17-MAR-1997  (first entry)
XX
DE   Human pancreatic alpha-amylase gene TFIID binding site.
XX
KW   Duplex DNA; target region; binding characteristic; DNA binding protein;
KW   TFIID; transcription factor; binding site; inhibition; enhance;
KW   cancer; inherited genetic disorder; ds.
```

XX
OS Homo sapiens.
XX
PN US5578444-A.
XX
PD 26-NOV-1996.
XX
PF 27-JUN-1991; 91US-0723618.
XX
PR 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1997-020402/02.
XX
PT Altering binding characteristics of DNA binding proteins to duplex
PT DNA - by attaching specific small cpd. to target region close to the
PT protein's binding site, useful in treatment of viral disease, cancer
PT etc
XX
PS Claim 6; Column 321-322; 264pp; English.
XX
CC The sequences given in AAT63713-4312 represent duplex DNA's which act
CC as target regions in the method of the invention. The method for
CC altering the binding characteristics of a DNA-binding protein to duplex
CC DNA comprises contacting the duplex DNA with a small molecule which
CC binds sequence-specifically to a target region, where, when the small
CC molecule is bound to the target region, it is adjacent to, but not
CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
CC The small molecule is added at a concentration effective to alter the
CC binding of the DNA binding protein, pref. TFIID, to its binding site on
CC the duplex DNA. The binding of the small molecule may inhibit or
CC enhance the binding of the DNA-binding protein to its binding site. The
CC compounds isolated using this method are potentially useful as
CC therapeutic agents for treatment of any disease which involves a
CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
CC The method is suitable for screening large biological or chemical
CC libraries and allows determination of sequence-specific and relative
CC affinities of known DNA-binding agents for different DNA sequences.
CC The design of these duplex DNA's allows a single DNA:protein interaction
CC to be used for screening sequence-specific, or preferential, DNA binding
CC proteins that recognise almost any possible sequence (see also AAT49539-
CC 74).
XX
SQ Sequence 50 BP; 18 A; 6 C; 10 G; 16 T; 0 other;

Query Match 74.0%; Score 14.8; DB 18; Length 50;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGCATATTCCTGTAAG 18
||| ||||||||||||
Db 32 TATTTATATTCCTGTAAG 15

RESULT 13
AAT64149/c
ID AAT64149 standard; DNA; 50 BP.
XX
AC AAT64149;
XX
DT 17-MAR-1997 (first entry)
XX
DE Human pancreatic amylase gene TFIID binding site.
XX
KW Duplex DNA; target region; binding characteristic; DNA binding protein;
KW TFIID; transcription factor; binding site; inhibition; enhance;
KW cancer; inherited genetic disorder; ds.

XX
OS Homo sapiens.
XX
PN US5578444-A.
XX
PD 26-NOV-1996.
XX
PF 27-JUN-1991; 91US-0723618.
XX
PR 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1997-020402/02.
XX
PT Altering binding characteristics of DNA binding proteins to duplex
PT DNA - by attaching specific small cpd. to target region close to the
PT protein's binding site, useful in treatment of viral disease, cancer
PT etc
XX
PS Claim 6; Column 321-322; 264pp; English.
XX
CC The sequences given in AAT63713-4312 represent duplex DNA's which act
CC as target regions in the method of the invention. The method for
CC altering the binding characteristics of a DNA-binding protein to duplex
CC DNA comprises contacting the duplex DNA with a small molecule which
CC binds sequence-specifically to a target region, where, when the small
CC molecule is bound to the target region, it is adjacent to, but not
CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
CC The small molecule is added at a concentration effective to alter the
CC binding of the DNA binding protein, pref. TFIID, to its binding site on
CC the duplex DNA. The binding of the small molecule may inhibit or
CC enhance the binding of the DNA-binding protein to its binding site. The
CC compounds isolated using this method are potentially useful as
CC therapeutic agents for treatment of any disease which involves a
CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
CC The method is suitable for screening large biological or chemical
CC libraries and allows determination of sequence-specific and relative
CC affinities of known DNA-binding agents for different DNA sequences.
CC The design of these duplex DNA's allows a single DNA:protein interaction
CC to be used for screening sequence-specific, or preferential, DNA binding
CC proteins that recognise almost any possible sequence (see also AAT49539-
CC 74).
XX
SQ Sequence 50 BP; 18 A; 6 C; 10 G; 16 T; 0 other;

Query Match 74.0%; Score 14.8; DB 18; Length 50;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGCATATTCCTGTAAG 18
||| ||||||||||||
Db 32 TATTTATATTCCTGTAAG 15

RESULT 14
AAX17436/c
ID AAX17436 standard; DNA; 50 BP.
XX
AC AAX17436;
XX
DT 06-MAY-1999 (first entry)
XX
DE Test sequence from human pancreatic alpha-amylase gene.
XX
KW Test sequence; DNA-binding molecule; screening sequence; human;
KW nucleic acid amplification; target; viral; ds.
XX

OS Homo sapiens.
XX
PN US5869241-A.
XX
PD 09-FEB-1999.
XX
PF 07-JUN-1995; 95US-0475228.
XX
PR 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
PR 07-JUN-1995; 95US-0475228.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1999-152755/13.
XX
PT Determination of DNA sequence preference of a DNA-binding molecule -
PT based on inhibition of binding of protein to oligonucleotide
PT sequence attached to test sequence
XX
PS Claim 3; Columns 323-324; 270pp; English.
XX
CC Sequences AAX17001 to AAX17600 represent specifically claimed target
CC test sequences that are used in the method of the invention of
CC determining the DNA sequence preference of a DNA-binding molecule. The
CC method comprises: (i) adding a test molecule and a DNA-binding protein to
CC a mixture of duplex DNA test oligonucleotides, each of the test
CC oligonucleotides having a test sequence adjacent to a screening sequence,
CC where the screening sequence binds to the DNA-binding protein with a
CC binding affinity that is independent of the DNA sequence of the test
CC sequence, and where the mixture of duplex DNA test oligonucleotides
CC includes several test sequences; (ii) incubating the test molecule, the
CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
CC for a time sufficient to permit binding of the test molecule to test
CC sequences in the duplex DNA; (iii) separating unbound test
CC oligonucleotides from test oligonucleotides bound to binding protein;
CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
CC (vii) sequencing the isolated test oligonucleotides. Test sequences
CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
CC genes and test sequences AAX17482-X17599 correspond to promoter targets
CC for viral genes.
XX
SQ Sequence 50 BP; 18 A; 6 C; 10 G; 16 T; 0 other;

Query Match 74.0%; Score 14.8; DB 20; Length 50;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGCATATTCCTGTAAG 18
||| ||||||||||||
Db 32 TATTTATATTCCTGTAAG 15

RESULT 15
AAX17437/c
ID AAX17437 standard; DNA; 50 BP.
XX
AC AAX17437;
XX
DT 06-MAY-1999 (first entry)
XX
DE Test sequence from human pancreatic amylase gene.
XX
KW Test sequence; DNA-binding molecule; screening sequence; human;
KW nucleic acid amplification; target; viral; ds.
XX
OS Homo sapiens.
XX
PN US5869241-A.
XX
PD 09-FEB-1999.
XX
PF 07-JUN-1995; 95US-0475228.
XX
PR 20-DEC-1993; 93US-0171389.
PR 27-JUN-1991; 91US-0723618.
PR 23-DEC-1992; 92US-0996783.
PR 17-SEP-1993; 93US-0123936.
PR 07-JUN-1995; 95US-0475228.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
XX
DR WPI; 1999-152755/13.
XX
PT Determination of DNA sequence preference of a DNA-binding molecule -
PT based on inhibition of binding of protein to oligonucleotide
PT sequence attached to test sequence
XX
PS Claim 3; Columns 323-324; 270pp; English.
XX
CC Sequences AAX17001 to AAX17600 represent specifically claimed target
CC test sequences that are used in the method of the invention of
CC determining the DNA sequence preference of a DNA-binding molecule. The
CC method comprises: (i) adding a test molecule and a DNA-binding protein to
CC a mixture of duplex DNA test oligonucleotides, each of the test
CC oligonucleotides having a test sequence adjacent to a screening sequence,
CC where the screening sequence binds to the DNA-binding protein with a
CC binding affinity that is independent of the DNA sequence of the test
CC sequence, and where the mixture of duplex DNA test oligonucleotides
CC includes several test sequences; (ii) incubating the test molecule, the
CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
CC for a time sufficient to permit binding of the test molecule to test
CC sequences in the duplex DNA; (iii) separating unbound test
CC oligonucleotides from test oligonucleotides bound to binding protein;
CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
CC (vii) sequencing the isolated test oligonucleotides. Test sequences
CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
CC genes and test sequences AAX17482-X17599 correspond to promoter targets
CC for viral genes.
XX
SQ Sequence 50 BP; 18 A; 6 C; 10 G; 16 T; 0 other;

Query Match 74.0%; Score 14.8; DB 20; Length 50;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TATGCATATTCCTGTAAG 18
||| ||||||||||||
Db 32 TATTTATATTCCTGTAAG 15

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GenCore version 5.1.3

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Perfect score: 20
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89787	A89787 Sequence 9
2		20	100.0	20	6	A90874	A90874 Sequence 9
3		20	100.0	20	6	AR078393	AR078393 Sequence
4		20	100.0	20	6	AX455575	AX455575 Sequence
5		20	100.0	27	6	AR063217	AR063217 Sequence
6		20	100.0	27	6	AX001643	AX001643 Sequence
7		20	100.0	27	6	I49528	I49528 Sequence 2
8		19	95.0	20	6	A89784	A89784 Sequence 6
9		19	95.0	20	6	A90871	A90871 Sequence 6
10		16.4	82.0	32	6	AR135319	AR135319 Sequence
11		16.4	82.0	50	6	AR032839	AR032839 Sequence
12		16.4	82.0	50	6	AR209503	AR209503 Sequence
13		16.4	82.0	50	6	I29579	I29579 Sequence 45
14		16.4	82.0	50	6	I91253	I91253 Sequence 45
15		15.8	79.0	20	6	A89786	A89786 Sequence 8
16		15.8	79.0	20	6	A90873	A90873 Sequence 8
17		14.4	72.0	83	6	AX328437	AX328437 Sequence
18	c	14.2	71.0	41	6	AR109119	AR109119 Sequence
19	c	14.2	71.0	41	6	AR200774	AR200774 Sequence
20		13.8	69.0	71	6	AR122803	AR122803 Sequence
21	c	13.6	68.0	51	6	AX162422	AX162422 Sequence
22		13.2	66.0	25	6	AX117480	AX117480 Sequence
23		13.2	66.0	51	6	AX117481	AX117481 Sequence
24		13.2	66.0	64	9	AF032251	AF032251 Otolemur
25	c	13.2	66.0	75	9	D86841S01	D86841 Homo sapien
26		13.2	66.0	76	9	AF032248	AF032248 Otolemur
27		13.2	66.0	76	9	AF032254	AF032254 Otolemur
28	c	13	65.0	26	6	A89779	A89779 Sequence 1
29	c	13	65.0	26	6	A90893	A90893 Sequence 28
30		12.8	64.0	21	6	A91594	A91594 Sequence 12
31	c	12.8	64.0	51	6	AX159923	AX159923 Sequence
32	c	12.8	64.0	51	6	AX159925	AX159925 Sequence
33	c	12.8	64.0	51	6	AX159926	AX159926 Sequence
34	c	12.8	64.0	51	6	AX160807	AX160807 Sequence
35	c	12.8	64.0	51	6	AX160808	AX160808 Sequence
36	c	12.8	64.0	51	6	AX164818	AX164818 Sequence
37		12.8	64.0	51	6	AX189849	AX189849 Sequence
38	c	12.8	64.0	61	6	AR118244	AR118244 Sequence
39		12.8	64.0	76	9	AF032239	AF032239 Otolemur
40		12.8	64.0	81	11	G34985	G34985 BPY1 human
41		12.6	63.0	57	6	AR064089	AR064089 Sequence
42	c	12.6	63.0	57	6	AR064090	AR064090 Sequence
43		12.6	63.0	57	6	BD008488	BD008488 Targeting
44	c	12.6	63.0	57	6	BD008489	BD008489 Targeting
45	c	12.6	63.0	58	6	AX053230	AX053230 Sequence

ALIGNMENTS

RESULT 1
A89787
LOCUS A89787 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 9 from Patent WO9832462.
ACCESSION A89787
VERSION A89787.1 GI:6738301
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 9 30-JUL-1998;

```
          LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      4 c      7 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
          ||||||||||||||||||||
Db      1 GATTGCCTGACGTCAGAGAG 20


RESULT 2
A90874
LOCUS       A90874                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 9 from Patent EP0855184.
ACCESSION   A90874
VERSION     A90874.1  GI:6739268
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 9 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
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Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      1 GATTGCCTGACGTCAGAGAG 20


RESULT 3
AR078393
LOCUS       AR078393                 20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 10 from patent US 5962636.
ACCESSION   AR078393
VERSION     AR078393.1  GI:10005139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bachmaier,K., Hessel,A.John., Neu,N. and Penninger,J.Martin.
  TITLE     Peptides capable of modulating inflammatory heart disease
  JOURNAL   Patent: US 5962636-A 10 05-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      4 c      7 g      4 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      1 GATTGCCTGACGTCAGAGAG 20


RESULT 4
AX455575
LOCUS       AX455575                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 52 from Patent WO0222809.
ACCESSION   AX455575
VERSION     AX455575.1  GI:21714643
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 52 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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BASE COUNT        5 a      4 c      7 g      4 t
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      1 GATTGCCTGACGTCAGAGAG 20


RESULT 5
AR063217
LOCUS       AR063217                 27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5844096.
ACCESSION   AR063217
VERSION     AR063217.1  GI:5990908
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hinrichs,S.H. and Orten,D.Jo.
  TITLE     Methods for inhibiting transcription of the cyclic AMP responsive
            element binding protein and the activating transcription factor 1
  JOURNAL   Patent: US 5844096-A 2 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        8 a      5 c      9 g      5 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 27;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 6
AX001643
LOCUS       AX001643                 27 bp    DNA     linear   PAT 10-MAR-2000
DEFINITION  Sequence 15 from Patent WO9856936.
ACCESSION   AX001643
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VERSION     AX001643.1  GI:7241772
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Damert,A. and Plate,K.
  TITLE     REGULATORY SEQUENCES INVOLVED IN HYPOXIA REGULATED GENE EXPRESSION
            AND USES THEREOF
  JOURNAL   Patent: WO 9856936-A 15 17-DEC-1998;
            MAX PLANCK GESELLSCHAFT (DE); DAMERT ANNETTE (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"
BASE COUNT        8 a      5 c      9 g      5 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 7
I49528
LOCUS       I49528                   27 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2 from patent US 5641486.
ACCESSION   I49528
VERSION     I49528.1  GI:2471748
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hinrichs,S.H. and Orten,D.Jo.
  TITLE     Methods for inhibiting transcription of the cyclic AMP responsive
            element binding protein and the activating transcription factor 1
  JOURNAL   Patent: US 5641486-A 2 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        8 a      5 c      9 g      5 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GATTGCCTGACGTCAGAGAG 20
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Db      4 GATTGCCTGACGTCAGAGAG 23


RESULT 8
A89784
LOCUS       A89784                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 6 from Patent WO9832462.
ACCESSION   A89784
VERSION     A89784.1  GI:6738298
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipford,G.B. and Heeg,K.
  TITLE     PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
            OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
  JOURNAL   Patent: WO 9832462-A 6 30-JUL-1998;
            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
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BASE COUNT        5 a      5 c      6 g      4 t
ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ATTGCCTGACGTCAGAGAG 20
          |||||||||||||||||||
Db      1 ATTGCCTGACGTCAGAGAG 19


RESULT 9
A90871
LOCUS       A90871                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 6 from Patent EP0855184.
ACCESSION   A90871
VERSION     A90871.1  GI:6739265
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 6 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      6 g      4 t
ORIGIN

  Query Match            95.0%;  Score 19;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 42;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ATTGCCTGACGTCAGAGAG 20
          |||||||||||||||||||
Db      1 ATTGCCTGACGTCAGAGAG 19


RESULT 10
AR135319
LOCUS       AR135319                 32 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6194632.
ACCESSION   AR135319
VERSION     AR135319.1  GI:14124224
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Leiden,J.M.
  TITLE     Mouse model for congestive heart failure
  JOURNAL   Patent: US 6194632-A 1 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
BASE COUNT        6 a      9 c     10 g      7 t
ORIGIN

  Query Match            82.0%;  Score 16.4;  DB 6;  Length 32;
  Best Local Similarity  94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 TTGCCTGACGTCAGAGAG 20
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Db      11 TTGGCTGACGTCAGAGAG 28


RESULT 11
AR032839
LOCUS       AR032839                  50 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 451 from patent US 5869241.
ACCESSION   AR032839
VERSION     AR032839.1  GI:5948444
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Method of determining DNA sequence preference of a DNA-binding
            molecule
  JOURNAL   Patent: US 5869241-A 451 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       17 a      7 c     18 g      8 t
ORIGIN

  Query Match             82.0%;  Score 16.4;  DB 6;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 9.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 TTGCCTGACGTCAGAGAG 20
          | ||||||||||||||||
Db      1 TAGCCTGACGTCAGAGAG 18


RESULT 12
AR209503
LOCUS       AR209503                  50 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 451 from patent US 6384208.
ACCESSION   AR209503
VERSION     AR209503.1  GI:21510946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence directed DNA binding molecules compositions and methods
  JOURNAL   Patent: US 6384208-A 451 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       17 a      7 c     18 g      8 t
ORIGIN

  Query Match             82.0%;  Score 16.4;  DB 6;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 9.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 TTGCCTGACGTCAGAGAG 20
          | ||||||||||||||||
Db      1 TAGCCTGACGTCAGAGAG 18


RESULT 13
I29579
LOCUS       I29579                    50 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 451 from patent US 5578444.
ACCESSION   I29579
VERSION     I29579.1  GI:1820370
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
  TITLE     Sequence-directed DNA-binding molecules compositions and methods
  JOURNAL   Patent: US 5578444-A 451 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       17 a      7 c     18 g      8 t
ORIGIN

  Query Match             82.0%;  Score 16.4;  DB 6;  Length 50;
  Best Local Similarity   94.4%;  Pred. No. 9.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 TTGCCTGACGTCAGAGAG 20
          | ||||||||||||||||
Db      1 TAGCCTGACGTCAGAGAG 18


RESULT 14
I91253
LOCUS       I91253                    50 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 451 from patent US 5726014.
ACCESSION   I91253
VERSION     I91253.1  GI:3935723
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
  TITLE     Screening assay for the detection of DNA-binding molecules
  JOURNAL   Patent: US 5726014-A 451 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       17 a      7 c     18 g      8 t
ORIGIN

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Qy      3 TTGCCTGACGTCAGAGAG 20
          | ||||||||||||||||
Db      1 TAGCCTGACGTCAGAGAG 18


RESULT 15
A89786
LOCUS       A89786                    20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 8 from Patent WO9832462.
ACCESSION   A89786
VERSION     A89786.1  GI:6738300
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipford,G.B. and Heeg,K.
  TITLE     PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
            OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
  JOURNAL   Patent: WO 9832462-A 8 30-JUL-1998;
            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      5 c      6 g      5 t
ORIGIN

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2 ATTGCCTGACGTCAGAGAG 20
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Db       1 ATTGCCTGACGTTCGAGAG 19
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Job time : 326.116 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
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Title: US-09-355-254F-21
Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89800	A89800 Sequence 22
2		20	100.0	20	6	A90887	A90887 Sequence 22
3		20	100.0	20	6	AR010171	AR010171 Sequence
4		20	100.0	20	6	AR204918	AR204918 Sequence
5		20	100.0	20	6	AR204923	AR204923 Sequence
6		20	100.0	20	6	AX455586	AX455586 Sequence
7		20	100.0	20	6	I33466	I33466 Sequence 3
8		20	100.0	20	6	I40053	I40053 Sequence 3
9		20	100.0	20	6	I47062	I47062 Sequence 3
10		20	100.0	20	6	I81487	I81487 Sequence 3
11		20	100.0	30	6	AR182577	AR182577 Sequence
12		20	100.0	42	6	A37863	A37863 Sequence 6
13		20	100.0	100	6	AR174601	AR174601 Sequence
14	c	20	100.0	100	6	AR174602	AR174602 Sequence
15		20	100.0	100	6	AX047032	AX047032 Sequence
16	c	20	100.0	100	6	AX047033	AX047033 Sequence
17		20	100.0	100	6	AX280202	AX280202 Sequence
18	c	20	100.0	100	6	AX280203	AX280203 Sequence
19		20	100.0	100	6	AX365191	AX365191 Sequence
20	c	20	100.0	100	6	AX365192	AX365192 Sequence
21	c	17	85.0	17	6	AR165233	AR165233 Sequence
22	c	17	85.0	17	6	AR201404	AR201404 Sequence
23	c	17	85.0	17	6	AX459960	AX459960 Sequence
24		17	85.0	17	6	I87794	I87794 Sequence 22
25		17	85.0	49	6	AR182576	AR182576 Sequence
26		16	80.0	25	6	AR083256	AR083256 Sequence
27		16	80.0	25	6	AR182574	AR182574 Sequence
28		16	80.0	30	6	AR048146	AR048146 Sequence
29		15.8	79.0	90	9	HSEXTR2	X99574 H.sapiens e
30	c	15	75.0	15	6	AX338644	AX338644 Sequence
31	c	15	75.0	15	6	I15312	I15312 Sequence 13
32	c	15	75.0	15	6	I31724	I31724 Sequence 13
33	c	15	75.0	15	6	I93568	I93568 Sequence 13
34	c	14.2	71.0	29	11	DOGCFTRC	L77689 Canis famil
35		14.2	71.0	39	10	MMVCAM1C7	U12877 Mus musculu
36	c	14.2	71.0	57	9	HSAPOLPA1	AF139730 Homo sapi
37	c	14.2	71.0	69	3	AF250305	AF250305 Chironomu
38		14.2	71.0	98	6	AX354846	AX354846 Sequence
39		14	70.0	16	6	AR165232	AR165232 Sequence
40		14	70.0	16	6	AR201403	AR201403 Sequence
41		14	70.0	16	6	AX338643	AX338643 Sequence
42		14	70.0	16	6	AX459959	AX459959 Sequence
43		14	70.0	16	6	I15311	I15311 Sequence 12
44		14	70.0	16	6	I31723	I31723 Sequence 12
45		14	70.0	16	6	I93567	I93567 Sequence 12

ALIGNMENTS

RESULT 1
A89800
LOCUS A89800 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 22 from Patent WO9832462.
ACCESSION A89800
VERSION A89800.1 GI:6738314
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 22 30-JUL-1998;

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          LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
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BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 2
A90887
LOCUS       A90887                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 22 from Patent EP0855184.
ACCESSION   A90887
VERSION     A90887.1  GI:6739333
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 22 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 3
AR010171
LOCUS       AR010171                 20 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756700.
ACCESSION   AR010171
VERSION     AR010171.1  GI:3968976
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hoey,T. and Rothe,M.
  TITLE     Nucleic acid encoding human signal transducer and activator of
            transcription 4
  JOURNAL   Patent: US 5756700-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .20
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BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 4
AR204918
LOCUS       AR204918                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 9 from patent US 6368828.
ACCESSION   AR204918
VERSION     AR204918.1  GI:21502366
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   LaRochelle,W., Patel,B.K.R. and Pierce,J.H.
  TITLE     Attenuated and dominant negative variant cDNAs of Stat6: Stat6b and
            Stat6c
  JOURNAL   Patent: US 6368828-A 9 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 5
AR204923
LOCUS       AR204923                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 14 from patent US 6368828.
ACCESSION   AR204923
VERSION     AR204923.1  GI:21502372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   LaRochelle,W., Patel,B.K.R. and Pierce,J.H.
  TITLE     Attenuated and dominant negative variant cDNAs of Stat6: Stat6b and
            Stat6c
  JOURNAL   Patent: US 6368828-A 14 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
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Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 6
AX455586
LOCUS       AX455586                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 63 from Patent WO0222809.
ACCESSION   AX455586
VERSION     AX455586.1  GI:21714654
KEYWORDS    .
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SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 63 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 7
I33466
LOCUS       I33466                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5591825.
ACCESSION   I33466
VERSION     I33466.1  GI:1824257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKnight,S.L. and Hou,J.
  TITLE     Interleukin 4 signal transducers
  JOURNAL   Patent: US 5591825-A 3 07-JAN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 8
I40053
LOCUS       I40053                   20 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 3 from patent US 5618693.
ACCESSION   I40053
VERSION     I40053.1  GI:2083058
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKnight,S.L., Hou,J. and Schindler,U.
  TITLE     Interleukin-2 signal transducers and binding assays
  JOURNAL   Patent: US 5618693-A 3 08-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 9
I47062
LOCUS       I47062                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5639858.
ACCESSION   I47062
VERSION     I47062.1  GI:2471027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hoey,T. and Rothe,M.
  TITLE     Human signal transducer and binding assays
  JOURNAL   Patent: US 5639858-A 3 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 10
I81487
LOCUS       I81487                   20 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 3 from patent US 5710266.
ACCESSION   I81487
VERSION     I81487.1  GI:3209784
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKnight,S.L. and Hou,J.
  TITLE     Nucleic acid encoding an interleukin 4 signal transducer
  JOURNAL   Patent: US 5710266-A 3 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      1 GTATTTCCCAGAAAAGGAAC 20


RESULT 11
AR182577
LOCUS       AR182577                 30 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 25 from patent US 6338949.
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ACCESSION   AR182577
VERSION     AR182577.1  GI:20225784
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Darnell,J.E. Jr., Schindler,C.W., Fu,X.-Y., Wen,Z. and Zhong,Z.
  TITLE     Nucleic acids encoding receptor recognition factor stat4 and
            methods of use thereof
  JOURNAL   Patent: US 6338949-A 25 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT       10 a      8 c      6 g      6 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 7.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db      6 GTATTTCCCAGAAAAGGAAC 25


RESULT 12
A37863
LOCUS       A37863                    42 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 6 from Patent WO9408025.
ACCESSION   A37863
VERSION     A37863.1  GI:2294543
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Benech,P., Perez,C. and Wietzerbin,J.
  TITLE     DNA SEQUENCES INVOLVED IN THE TRANSCRIPTION OF GENES UNDER THE
            EFFECT OF INDUCERS, AND BIOLOGICAL APPLICATIONS THEREOF
  JOURNAL   Patent: WO 9408025-A 6 14-APR-1994;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication FR 2696181 940401.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       14 a      6 c     10 g     12 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 42;
  Best Local Similarity  100.0%;  Pred. No. 7.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db     23 GTATTTCCCAGAAAAGGAAC 42


RESULT 13
AR174601
LOCUS       AR174601                  100 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 59 from patent US 6307024.
ACCESSION   AR174601
VERSION     AR174601.1  GI:17914921
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 59 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="unknown"
BASE COUNT       25 a      32 c      17 g      26 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 8.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db     44 GTATTTCCCAGAAAAGGAAC 63


RESULT 14
AR174602/c
LOCUS       AR174602                  100 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 60 from patent US 6307024.
ACCESSION   AR174602
VERSION     AR174602.1  GI:17914922
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 60 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="unknown"
BASE COUNT       26 a      17 c      32 g      25 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 8.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTATTTCCCAGAAAAGGAAC 20
          ||||||||||||||||||||
Db     61 GTATTTCCCAGAAAAGGAAC 42


RESULT 15
AX047032
LOCUS       AX047032                  100 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 37 from Patent WO0068381.
ACCESSION   AX047032
VERSION     AX047032.1  GI:11876456
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse zcytor10
  JOURNAL   Patent: WO 0068381-A 37 16-NOV-2000;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a      33 c      17 g      26 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 8.3;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GTATTTCCCAGAAAAGGAAC 20
           ||||||||||||||||||||
Db      44 GTATTTCCCAGAAAAGGAAC 63
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89799	A89799 Sequence 21
2		20	100.0	20	6	A90886	A90886 Sequence 21
3		20	100.0	20	6	AX455553	AX455553 Sequence
4		20	100.0	21	6	I23456	I23456 Sequence 8
5		20	100.0	100	6	AR174601	AR174601 Sequence
6	c	20	100.0	100	6	AR174602	AR174602 Sequence
7		20	100.0	100	6	AX047032	AX047032 Sequence
8	c	20	100.0	100	6	AX047033	AX047033 Sequence
9		20	100.0	100	6	AX280202	AX280202 Sequence
10	c	20	100.0	100	6	AX280203	AX280203 Sequence
11		20	100.0	100	6	AX365191	AX365191 Sequence
12	c	20	100.0	100	6	AX365192	AX365192 Sequence
13	c	14.2	71.0	31	6	AR119638	AR119638 Sequence
14	c	14.2	71.0	31	6	AR169119	AR169119 Sequence
15		14.2	71.0	58	6	AR138229	AR138229 Sequence
16	c	14.2	71.0	64	12	SYNECOCGK	K01192 Yeast (S.ce
17	c	13.8	69.0	24	6	A03717	A03717 Oligonucleo
18	c	13.8	69.0	41	6	AX343814	AX343814 Sequence
19	c	13.8	69.0	41	6	AX343816	AX343816 Sequence
20	c	13.8	69.0	44	6	AX343812	AX343812 Sequence
21	c	13.8	69.0	44	6	AX343818	AX343818 Sequence
22	c	13.8	69.0	76	8	YSCGENC152	M87429 Yeast Eco R
23		13.8	69.0	91	1	AF087321	AF087321 Chlamydia
24		13.8	69.0	94	10	AY041972	AY041972 Phodopus
25	c	13.6	68.0	25	6	AR043941	AR043941 Sequence
26	c	13.6	68.0	25	6	AR073474	AR073474 Sequence
27	c	13.6	68.0	25	6	AX022068	AX022068 Sequence
28	c	13.6	68.0	25	6	I93345	I93345 Sequence 15
29	c	13.6	68.0	26	6	AR043992	AR043992 Sequence
30	c	13.6	68.0	26	6	AR073525	AR073525 Sequence
31	c	13.6	68.0	26	6	AX022135	AX022135 Sequence
32	c	13.6	68.0	26	6	I93396	I93396 Sequence 82
33		13.6	68.0	65	6	AX483015	AX483015 Sequence
34	c	13.6	68.0	72	6	AR043980	AR043980 Sequence
35	c	13.6	68.0	72	6	AR073513	AR073513 Sequence
36	c	13.6	68.0	72	6	AX022123	AX022123 Sequence
37	c	13.6	68.0	72	6	I93384	I93384 Sequence 70
38	c	13.2	66.0	31	6	AX327657	AX327657 Sequence
39		13.2	66.0	45	6	AR076832	AR076832 Sequence
40	c	13.2	66.0	51	6	AX160107	AX160107 Sequence
41		13.2	66.0	58	6	AR140194	AR140194 Sequence
42		13.2	66.0	58	6	AR173275	AR173275 Sequence
43		13.2	66.0	63	6	AR138221	AR138221 Sequence
44	c	13.2	66.0	72	6	I74780	I74780 Sequence 12
45	c	13.2	66.0	74	10	RATPAM25	U52661 Rattus norv

ALIGNMENTS

RESULT 1
A89799
LOCUS A89799 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 21 from Patent WO9832462.
ACCESSION A89799
VERSION A89799.1 GI:6738313
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 21 30-JUL-1998;

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          LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      3 c      3 g      7 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAATC 20


RESULT 2
A90886
LOCUS       A90886                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 21 from Patent EP0855184.
ACCESSION   A90886
VERSION     A90886.1  GI:6739328
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 21 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      3 c      3 g      7 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAATC 20


RESULT 3
AX455553
LOCUS       AX455553                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 30 from Patent WO0222809.
ACCESSION   AX455553
VERSION     AX455553.1  GI:21714621
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 30 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        7 a      3 c      3 g      7 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAATC 20


RESULT 4
I23456
LOCUS       I23456                   21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 8 from patent US 5534409.
ACCESSION   I23456
VERSION     I23456.1  GI:1603326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Groner,B., Gouilleux,F. and Wakao,H.
  TITLE     Cytokine regulated transcription factor
  JOURNAL   Patent: US 5534409-A 8 09-JUL-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        7 a      4 c      3 g      7 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAATC 20


RESULT 5
AR174601
LOCUS       AR174601                100 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 59 from patent US 6307024.
ACCESSION   AR174601
VERSION     AR174601.1  GI:17914921
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 59 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="unknown"
BASE COUNT       25 a     32 c     17 g     26 t
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAATC 86


RESULT 6
AR174602/c
LOCUS       AR174602                100 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 60 from patent US 6307024.
```

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ACCESSION   AR174602
VERSION     AR174602.1  GI:17914922
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 60 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="unknown"
BASE COUNT       26 a     17 c     32 g     25 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAATC 19


RESULT 7
AX047032
LOCUS       AX047032                100 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 37 from Patent WO0068381.
ACCESSION   AX047032
VERSION     AX047032.1  GI:11876456
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse zcytor10
  JOURNAL   Patent: WO 0068381-A 37 16-NOV-2000;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a     33 c     17 g     26 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAATC 86


RESULT 8
AX047033/c
LOCUS       AX047033                100 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 38 from Patent WO0068381.
ACCESSION   AX047033
VERSION     AX047033.1  GI:11876457
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse zcytor10
  JOURNAL   Patent: WO 0068381-A 38 16-NOV-2000;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12748"
BASE COUNT       26 a     17 c     33 g     24 t
ORIGIN

  Query Match           100.0%;  Score 20;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAATC 19


RESULT 9
AX280202
LOCUS       AX280202                100 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 48 from Patent WO0177171.
ACCESSION   AX280202
VERSION     AX280202.1  GI:16607595
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Novak,J.E., West,J.W., Presnell,S.R., Holly,R.D. and
            Nelson,A.J.
  TITLE     Soluble zalpha11 cytokine receptors
  JOURNAL   Patent: WO 0177171-A 48 18-OCT-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a     33 c     17 g     26 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAATC 86


RESULT 10
AX280203/c
LOCUS       AX280203                100 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 49 from Patent WO0177171.
ACCESSION   AX280203
VERSION     AX280203.1  GI:16607596
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Novak,J.E., West,J.W., Presnell,S.R., Holly,R.D. and
            Nelson,A.J.
  TITLE     Soluble zalpha11 cytokine receptors
  JOURNAL   Patent: WO 0177171-A 49 18-OCT-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12748"
BASE COUNT       26 a     17 c     33 g     24 t
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ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAATC 19


RESULT 11
AX365191
LOCUS       AX365191                100 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 43 from Patent WO0200721.
ACCESSION   AX365191
VERSION     AX365191.1  GI:18696947
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L.
            and Maurer,M.F.
  TITLE     Cytokine receptor zcytor17
  JOURNAL   Patent: WO 0200721-A 43 03-JAN-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a     33 c     17 g     26 t
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAATC 86


RESULT 12
AX365192/c
LOCUS       AX365192                100 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 44 from Patent WO0200721.
ACCESSION   AX365192
VERSION     AX365192.1  GI:18696948
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L.
            and Maurer,M.F.
  TITLE     Cytokine receptor zcytor17
  JOURNAL   Patent: WO 0200721-A 44 03-JAN-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12748"
BASE COUNT       26 a     17 c     33 g     24 t
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAATC 20
          ||||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAATC 19


RESULT 13
AR119638/c
LOCUS       AR119638                31 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 30 from patent US 6153397.
ACCESSION   AR119638
VERSION     AR119638.1  GI:14102337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Wisnewski,N., Silver,G.M., Lo,K.Callies. and Brandt,K.S.
  TITLE     Flea epoxide hydrolase proteins and uses thereof
  JOURNAL   Patent: US 6153397-A 30 28-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        7 a      6 c      5 g     13 t
ORIGIN

  Query Match            71.0%;  Score 14.2;  DB 6;  Length 31;
  Best Local Similarity  84.2%;  Pred. No. 1.5e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAT 19
          |||| |||  |||||||||
Db     19 AGATCTCTGAGAATTCAAT 1


RESULT 14
AR169119/c
LOCUS       AR169119                31 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6290958.
ACCESSION   AR169119
VERSION     AR169119.1  GI:17906878
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Wisnewski,N., Silver,G.M., Lo,K.Callies. and Brandt,K.S.
  TITLE     Anti-flea epoxide hydrolase antibodies and uses thereof
  JOURNAL   Patent: US 6290958-A 30 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        7 a      6 c      5 g     13 t
ORIGIN

  Query Match            71.0%;  Score 14.2;  DB 6;  Length 31;
  Best Local Similarity  84.2%;  Pred. No. 1.5e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAT 19
          |||| |||  |||||||||
Db     19 AGATCTCTGAGAATTCAAT 1


RESULT 15
AR138229
LOCUS       AR138229                58 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 46 from patent US 6197930.
ACCESSION   AR138229
VERSION     AR138229.1  GI:14479738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 58)
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```
  AUTHORS   Sheppard,P.O. and Humes,J.M.
  TITLE     Adipocyte-specific protein homologs
  JOURNAL   Patent: US 6197930-A 46 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="unknown"
BASE COUNT       17 a      16 c       9 g      16 t
ORIGIN

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  Best Local Similarity   84.2%;  Pred. No. 1.2e+05;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 AGATTTCTAGGAATTCAAT 19
           ||| | |||||||||| ||
Db      14 AGAATACTAGGAATTCTAT 32


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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 01:06:16 ; Search time 318.116 Seconds
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Title: US-09-355-254F-19
Perfect score: 20
Sequence: 1 ctgatttccccgaaatgatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	6	A89798	A89798 Sequence 20
2		20	100.0	20	6	A90885	A90885 Sequence 20
3		20	100.0	20	6	AX455567	AX455567 Sequence
4	c	20	100.0	21	6	I39725	I39725 Sequence 12
5	c	20	100.0	21	6	I55842	I55842 Sequence 12
6		18	90.0	86	6	AR184059	AR184059 Sequence
7		18	90.0	86	6	AR203344	AR203344 Sequence
8		18	90.0	86	6	AR206966	AR206966 Sequence
9		16.4	82.0	22	6	AR062163	AR062163 Sequence
10		15.2	76.0	24	6	AR061864	AR061864 Sequence
11		15	75.0	19	6	AR043736	AR043736 Sequence
12	c	15	75.0	19	6	AR043737	AR043737 Sequence
13		15	75.0	19	6	I81940	I81940 Sequence 38
14	c	15	75.0	19	6	I81941	I81941 Sequence 39
15	c	13.8	69.0	27	3	AF251713S4	AF251716 Acerentom
16	c	13.8	69.0	27	3	AF251718S4	AF251721 Orchesell
17	c	13.8	69.0	27	3	AF251743S4	AF251746 Tomocerus
18		13.8	69.0	65	6	AX485415	AX485415 Sequence
19	c	13.6	68.0	41	6	AX088050	AX088050 Sequence
20	c	13.6	68.0	51	6	AX115257	AX115257 Sequence
21	c	13.6	68.0	100	1	ECOFIMPHC	M11776 E.coli inve
22		13.4	67.0	20	6	AR208137	AR208137 Sequence
23	c	13.4	67.0	60	6	AR009405	AR009405 Sequence
24	c	13.4	67.0	90	3	PFASSRR	D17580 Plasmodium
25	c	13.4	67.0	90	6	AR022104	AR022104 Sequence
26	c	13.4	67.0	90	6	AR022120	AR022120 Sequence
27	c	13.4	67.0	90	6	E08156	E08156 Primer or p
28		13.2	66.0	28	6	I39716	I39716 Sequence 3
29		13.2	66.0	28	6	I55833	I55833 Sequence 3
30		13.2	66.0	35	6	A92293	A92293 Sequence 12
31		13.2	66.0	35	6	A92344	A92344 Sequence 12
32		13.2	66.0	35	6	BD007234	BD007234 Lentiviru
33	c	13.2	66.0	38	6	I15748	I15748 Sequence 14
34	c	13.2	66.0	41	6	AX088048	AX088048 Sequence
35	c	13.2	66.0	48	6	AX429820	AX429820 Sequence
36	c	13.2	66.0	83	12	AY096764	AY096764 Populus t
37		13.2	66.0	90	10	RAT11BHYSD	M77835 R.norvegicu
38		13	65.0	13	6	AX026535	AX026535 Sequence
39		12.8	64.0	20	6	AX296543	AX296543 Sequence
40		12.8	64.0	24	6	AX291910	AX291910 Sequence
41	c	12.8	64.0	27	3	AF251728S4	AF251731 Dicyrtoma
42	c	12.8	64.0	27	3	AF251738S4	AF251741 Bilobella
43	c	12.8	64.0	48	9	HSA308535	AJ308535 Homo sapi
44	c	12.8	64.0	49	6	A43525	A43525 Sequence 5
45	c	12.8	64.0	49	6	AR052464	AR052464 Sequence

ALIGNMENTS

RESULT 1
A89798
LOCUS A89798 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 20 from Patent WO9832462.
ACCESSION A89798
VERSION A89798.1 GI:6738312
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 20 30-JUL-1998;

LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES Location/Qualifiers
source 1. .20
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATTTCCCCGAAATGATG 20
||||||||||||||||||||
Db 1 CTGATTTCCCCGAAATGATG 20

RESULT 2
A90885
LOCUS A90885 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 20 from Patent EP0855184.
ACCESSION A90885
VERSION A90885.1 GI:6739323
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Heeg,K.P. and Lipford,G.B.
TITLE Pharmaceutical composition comprising a polynucleotide and an antigen especially for vaccination
JOURNAL Patent: EP 0855184-A 20 29-JUL-1998;
HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES Location/Qualifiers
source 1. .20
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 5 a 5 c 4 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATTTCCCCGAAATGATG 20
||||||||||||||||||||
Db 1 CTGATTTCCCCGAAATGATG 20

RESULT 3
AX455567
LOCUS AX455567 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 44 from Patent WO0222809.
ACCESSION AX455567
VERSION AX455567.1 GI:21714635
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bauer,S., Lipford,G. and Wagner,H.
TITLE Process for high throughput screening of cpg-based immuno-agonist/antagonist
JOURNAL Patent: WO 0222809-A 44 21-MAR-2002;
Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
BASE COUNT 5 a 5 c 4 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATTTCCCCGAAATGATG 20
||||||||||||||||||||
Db 1 CTGATTTCCCCGAAATGATG 20

RESULT 4
I39725/c
LOCUS I39725 21 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 12 from patent US 5616489.
ACCESSION I39725
VERSION I39725.1 GI:2084205
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Levy,D.E.
TITLE DNA sequence which binds transcriptional regulatory proteins activated in response to various cytokines and uses thereof
JOURNAL Patent: US 5616489-A 12 01-APR-1997;
FEATURES Location/Qualifiers
source 1. .21
/organism="unknown"
BASE COUNT 6 a 4 c 6 g 5 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATTTCCCCGAAATGATG 20
||||||||||||||||||||
Db 20 CTGATTTCCCCGAAATGATG 1

RESULT 5
I55842/c
LOCUS I55842 21 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 12 from patent US 5648217.
ACCESSION I55842
VERSION I55842.1 GI:2476636
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Levy,D.E.
TITLE DNA sequence which binds transcriptional regulatory proteins activated in response to various cytokines and uses thereof
JOURNAL Patent: US 5648217-A 12 15-JUL-1997;
FEATURES Location/Qualifiers
source 1. .21
/organism="unknown"
BASE COUNT 6 a 4 c 6 g 5 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATTTCCCCGAAATGATG 20
||||||||||||||||||||
Db 20 CTGATTTCCCCGAAATGATG 1

RESULT 6
AR184059
LOCUS AR184059 86 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3 from patent US 6342581.

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ACCESSION   AR184059
VERSION     AR184059.1  GI:20228028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Rosen,C.A., Ruben,S.M., Olsen,H.S. and Ebner,R.
  TITLE     Secreted protein HLHFP03
  JOURNAL   Patent: US 6342581-A 3 29-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .86
                     /organism="unknown"
BASE COUNT       23 a      26 c      13 g      24 t
ORIGIN

  Query Match             90.0%;  Score 18;  DB 6;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TGATTTCCCCGAAATGAT 19
          ||||||||||||||||||
Db     40 TGATTTCCCCGAAATGAT 57


RESULT 7
AR203344
LOCUS       AR203344                  86 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6365369.
ACCESSION   AR203344
VERSION     AR203344.1  GI:21499709
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Endress,G.A. and Rosen,C.A.
  TITLE     Prostate specific secreted protein
  JOURNAL   Patent: US 6365369-A 6 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .86
                     /organism="unknown"
BASE COUNT       23 a      26 c      13 g      24 t
ORIGIN

  Query Match             90.0%;  Score 18;  DB 6;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TGATTTCCCCGAAATGAT 19
          ||||||||||||||||||
Db     40 TGATTTCCCCGAAATGAT 57


RESULT 8
AR206966
LOCUS       AR206966                  86 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 18 from patent US 6372473.
ACCESSION   AR206966
VERSION     AR206966.1  GI:21505728
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Moore,P.A., Ruben,S.M. and Ebner,R.
  TITLE     Tissue plasminogen activator-like protease
  JOURNAL   Patent: US 6372473-A 18 16-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .86
                     /organism="unknown"
BASE COUNT       23 a      26 c      13 g      24 t
ORIGIN

  Query Match             90.0%;  Score 18;  DB 6;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TGATTTCCCCGAAATGAT 19
          ||||||||||||||||||
Db     40 TGATTTCCCCGAAATGAT 57


RESULT 9
AR062163
LOCUS       AR062163                  22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 24 from patent US 5843697.
ACCESSION   AR062163
VERSION     AR062163.1  GI:5989854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Pestka,S. and Kotenko,S.V.
  TITLE     Cells expressing IL-10 receptor and the CRFB4 gene product, an
            IL-10 receptor accessory protein
  JOURNAL   Patent: US 5843697-A 24 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a       6 c       4 g       6 t
ORIGIN

  Query Match             82.0%;  Score 16.4;  DB 6;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 3.5e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 GATTTCCCCGAAATGATG 20
          |||||||||||||| |||
Db      5 GATTTCCCCGAAATCATG 22


RESULT 10
AR061864
LOCUS       AR061864                  24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 56 from patent US 5843660.
ACCESSION   AR061864
VERSION     AR061864.1  GI:5989555
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Schumm,J.W., Micka,K.A. and Rabbach,D.R.
  TITLE     Multiplex amplification of short tandem repeat loci
  JOURNAL   Patent: US 5843660-A 56 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        5 a       6 c       4 g       9 t
ORIGIN

  Query Match             76.0%;  Score 15.2;  DB 6;  Length 24;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CTGATTTCCCCGAAATGATG 20
          || |||| |||| |||||||
Db      5 CTCATTTTCCCGCAATGATG 24


RESULT 11
AR043736
LOCUS       AR043736                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 106 from patent US 5814517.
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ACCESSION   AR043736
VERSION     AR043736.1  GI:5964744
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 106 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      5 c      4 g      5 t
ORIGIN

  Query Match           75.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GATTTCCCCGAAATG 17
          |||||||||||||||
Db      5 GATTTCCCCGAAATG 19


RESULT 12
AR043737/c
LOCUS       AR043737                19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 107 from patent US 5814517.
ACCESSION   AR043737
VERSION     AR043737.1  GI:5964745
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 107 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      4 c      5 g      5 t
ORIGIN

  Query Match           75.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GATTTCCCCGAAATG 17
          |||||||||||||||
Db     19 GATTTCCCCGAAATG 5


RESULT 13
I81940
LOCUS       I81940                  19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 38 from patent US 5712094.
ACCESSION   I81940
VERSION     I81940.1  GI:3210237
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
  TITLE     Methods for detecting modulators of cytokine action
  JOURNAL   Patent: US 5712094-A 38 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      5 c      4 g      5 t
ORIGIN

  Query Match           75.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GATTTCCCCGAAATG 17
          |||||||||||||||
Db      5 GATTTCCCCGAAATG 19


RESULT 14
I81941/c
LOCUS       I81941                  19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 39 from patent US 5712094.
ACCESSION   I81941
VERSION     I81941.1  GI:3210238
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Seidel,H.Martin., Lamb,I.Peter. and Chan,S.-S.Tian.
  TITLE     Methods for detecting modulators of cytokine action
  JOURNAL   Patent: US 5712094-A 39 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      4 c      5 g      5 t
ORIGIN

  Query Match           75.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GATTTCCCCGAAATG 17
          |||||||||||||||
Db     19 GATTTCCCCGAAATG 5


RESULT 15
AF251713S4/c
LOCUS       AF251713S4              27 bp    DNA     linear   INV 12-OCT-2000
DEFINITION  Acerentomon sp. CFNDS1 elongation factor 1-alpha gene, exon 4.
ACCESSION   AF251716
VERSION     AF251716.1  GI:10798923
KEYWORDS    .
SEGMENT     4 of 5
SOURCE      Acerentomon sp. CFNDS1.
  ORGANISM  Acerentomon sp. CFNDS1
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Protura; Acerentomoidea;
            Acerentomidae; Acerentomon.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Carapelli,A., Frati,F., Nardi,F., Dallai,R. and Simon,C.
  TITLE     Molecular phylogeny of the Apterygotan insects based on nuclear and
            mitochondrial genes
  JOURNAL   Pedobiologia (Jena) 44, 361-373 (2000)
REFERENCE   2  (bases 1 to 27)
  AUTHORS   Carapelli,A., Frati,F., Nardi,F., Dallai,R. and Simon,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2000) Evolutionary Biology, University of Siena,
            via P.A. Mattioli 4, Siena 53100, Italy
COMMENT     Region: Presence of introns of unknown lenght between  s 1&2, 2&3,
            3&4.
            Region: The five  s joined together correspond to bases 2108 to
            2617 in Drosophila melanogaster F1 sequence (accession X06869).
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Acerentomon sp. CFNDS1"
                     /db_xref="taxon:135967"
     exon            1. .27
                     /number=4
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BASE COUNT 10 a 4 c 8 g 5 t
ORIGIN

Query Match 69.0%; Score 13.8; DB 3; Length 27;
Best Local Similarity 88.2%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2 TGATTTCCCCGAAATGA 18
           ||||||||  |||||  ||
Db      19 TGATTTCCTCGAAACGA 3
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Search completed: December 12, 2002, 02:56:06
Job time : 322.116 secs